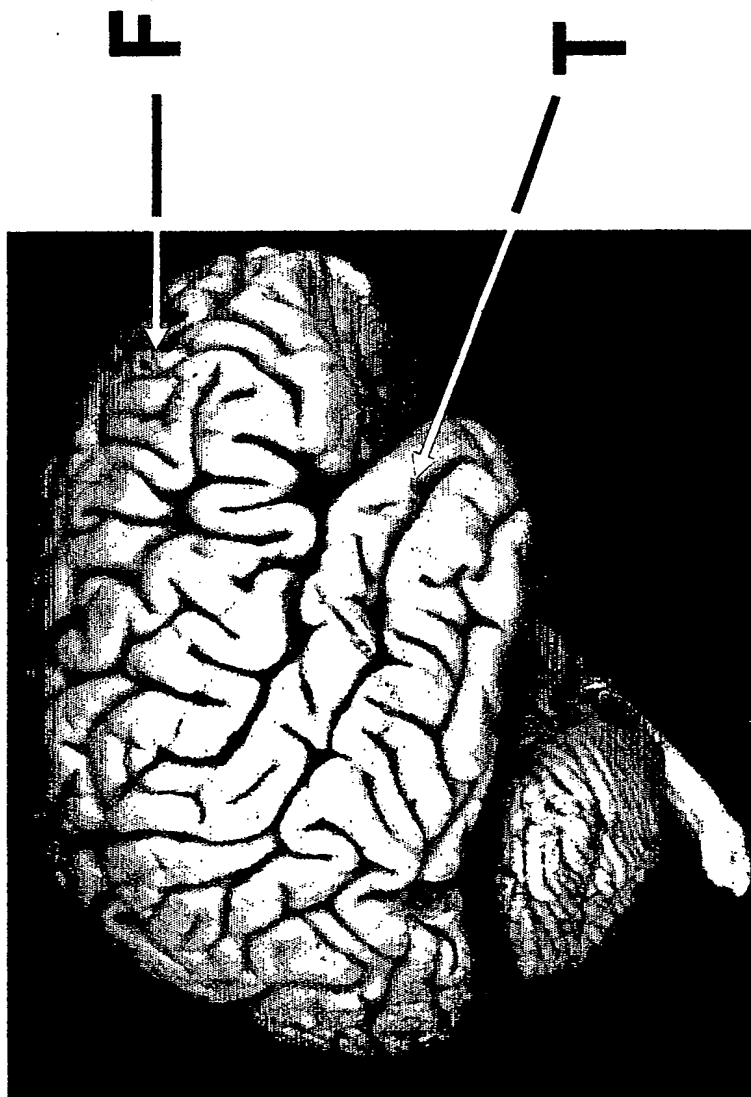


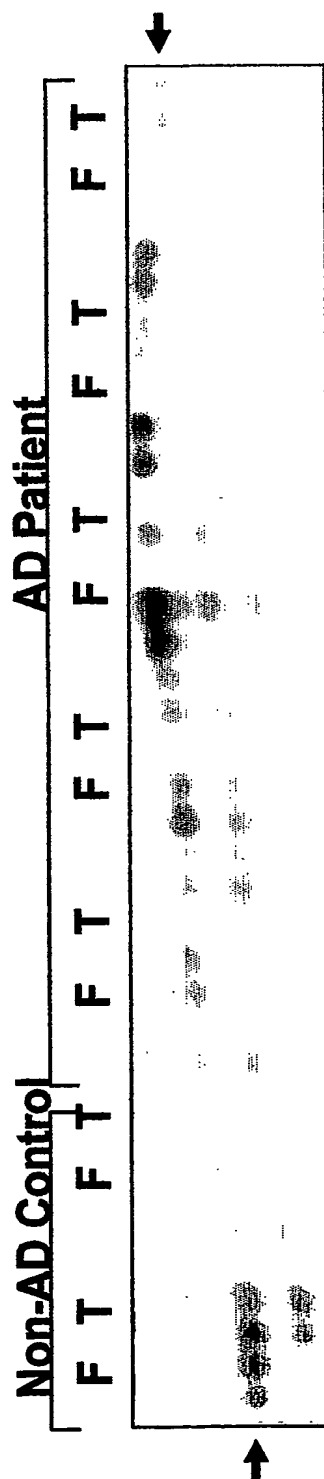
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**Fig. 1: Identification of Genes Involved
in Alzheimer's Disease Pathology**



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**Fig. 2: Identification of differentially expressed genes
in a fluorescence differential display screen**



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Figure 3: SEQ ID NO. 1

Length: 36 bp

1 AGTTAAGTTT CTTTGTA AAA CACTGATTTT TTCTCC

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Fig. 4: Alignment of SEQ ID NO. 1 with human golgin-245 cDNA (GenBank accession number U41740)

```
36 GGAGAAAAAATCAGTGTTTTACAAAGAACTTAACT 1
   | | | | | | | | | | | | | | | | | | | | | |
5488 GAAGAAAAAATCAGTGTTTTACAAAGAACTTAACT 5523
```

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Fig. 5: SEQ ID NO. 2: amino acid sequence of human golgin-245, splice variant 1**Length: 2228 aa**

1	MFKKLKQKIS	EEQQQLQQAL	APAQASSNSS	TPTRMRSRTS	SFTEQLDEGT
51	PNRESGDTQS	FAQKLQLRVP	SVESLFRSPI	KESLFRSSSK	ESLVRTSSRE
101	SLNRLDLDS	TASFDPPSDM	DSEAEDLVGN	SDSLNKEQLI	QRLRRMERSL
151	SSYRGKYSEL	VTAYQMLQRE	KKKLQGILSQ	SQDKSLRRIA	ELREELQMDQ
201	QAKKHLQEEF	DASLEEKDQY	ISVLQTQVSL	LKQRLRNGPM	NVDVLKPLPQ
251	LEPQAEVFTK	EENPESDGEP	VVEDGTSVKT	LETLOQRVVKR	QENLLKRCKE
301	TIQSHKEQCT	LLTSEKEALQ	EQLDERLQEL	EKIKDLHMAE	KTKLITQLRD
351	AKNLIEQLEQ	DKGMVIAETK	RQMHELTLEMK	EEEIAQLRSR	IKQMTTQGEE
401	LREQKEKSER	AAFEELEKAL	STAQKTEEAR	RKLKAEMDEQ	IKTIEKTSEE
451	ERISLQQELS	RVKQEVVDVM	KKSSEEQIAK	LQKLHEKELA	RKEQELTKKL
501	QTREREFQEQ	MKVALEKSQS	EYLIKISQEK	QQESLALIEL	ELQKKAILTE
551	SENKLRLDQQ	EAETYRTRIL	ELESSLEKSL	QENKNQSKDL	AVHLEAEKNK
601	HNKEITVMVE	KHKTELESLE	HQODALWTEK	LQVLKQQYQT	EMEKLREKCE
651	QEKETLLKDK	EIIFQAHIEE	MNEKTLEKLD	VKQTELESLS	SELSEVLKAR
701	HKLEEEELSVL	KDQTDKMKQE	LEAKMDEQKN	HHQQQVDSII	KEHEVSIQRT
751	EKALKDQINQ	LELLLLKERDK	HLKEHQAHVE	NLEADIKRSE	GELQQASAKL
801	DVFQSYQSAT	HEQTKAYEEQ	LAQLQOKLLD	LETERILLTK	QVAEVEAQKK
851	DVCTELDAHK	IQVQDLMQQL	EKQNSEMEQK	VKSLTQVYES	KLEDGNKEQE
901	QTKQILVEKE	NMILQMREGQ	KKEIEILTQK	LSAKEDSIHI	LNEEYETKFK
951	NQEKKMEKVK	QKAKEMQETL	KKKLLDQEAK	LKKELENTAL	ELSQKEKQFN
1001	AKMLEMAQAN	SAGISDAVSR	LETNQKEQIE	SLTEVHRREL	NDVISIWEKK
1051	LNQQAEELQE	IHEIQLOEKE	QEVaelKQKI	LLFGCEKEEM	NKEITWLKEE
1101	GVKQDITLNE	LQEQLKQKSA	HVNSLAQDET	KLKAHLEKLE	VDLNKSLKEN
1151	TFLQEQLVEL	KMLAEEDKRR	VSELTSLKKT	TDEEFQSLKS	SHEKSNKSLE
1201	DKSLEFFKLS	EELAIQLDIC	CKKTEALLEA	KTNELINISS	SKTNAILSRI
1251	SHCQHRTTKV	KEALLIKTCT	VSELEAQLRQ	LTEEQNTLNI	SFQQATHQLE
1301	EKENQIKSMK	ADIESLVTEK	EALQKEGGNQ	QQAASEKESC	ITQLKKELSE
1351	NINAVTLMKE	ELKEKKVEIS	SLSKQLTDLN	VQLQNSISLS	EKEAAISSLR
1401	KQYDEEKCEL	LDQVQDLSFK	VDTLSKEKIS	ALEQVDDWSN	KFSEWKKAQ
1451	SRFTQHONTV	KELQIQLELK	SKEAYEKDEQ	INLLKEELDQ	QNKRFDCCLKG
1501	EMEDDKSKME	KKESNLETET	KSQTARIMEL	EDHITQKTIE	IESLNEVLKN
1551	YNQQKDIEHK	ELVQKLQHFQ	ELGEEKDNRV	KEAEEKILTL	ENQVYSMAE
1601	LETKKKELEH	VNLSVKSKEE	ELKALEDRL	SESAAKLAEL	KRKAQEKIAA
1651	IKKQLLSQME	EKEEQYKKGT	ESHLSELNTK	LQEREREVHI	LEEKLSVES
1701	SQSETLIVPR	SAKNVAAYTE	QEEADSQGCV	QKTYEEKISV	LQRNLTEKEK
1751	LLQRVGQEKE	ETVSSHFEMR	CQYQERLIKL	EHAQAKQHED	QSMIGHLQEE
1801	LEEKNNKYSL	IVAQHVEKEG	GKNNIQAKQN	LENVFDDVQK	TLQEKELTCQ
1851	ILEQKIKELD	SCLVRQKEVH	RVEMEELTSK	YEKLQALQQM	DGRNKPTELL
1901	EENTEEKSKS	HLVQPKLLSN	MEAQHNDFEF	KLGAEREKQ	KLKGEIVRLQ
1951	KDLRMLRKEH	QQELEILKKE	YDQEREKIK	QELEDLELKH	NSTLQQLMRE
2001	FNTQLAQKEQ	ELEMTIKETI	NKAQVEAEAL	LESHQEETNQ	LLKKIAEKDD
2051	DLKRTAKRYE	EILDAREEEM	TAKVRDLQTO	LEELQKKYQQ	KLEQEENPGN
2101	DNVTIMELQT	QLAQKTTLIS	DSKLKEQEFR	EQIHNLEDRL	KKYEKNVYAT
2151	TVGTPYKGGN	LYHTDVSLEF	EPTEFEYLRK	VLFEYMMGRE	TKTMAKVITT
2201	VLKFPDDQTQ	KILEREARL	MSWLRSSS		

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Fig. 6: SEQ ID NO. 3: nucleotide sequence of human golgin-245 cDNA, splice variant 1

Length: 7636 bp

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1   GCAACGAAGG TACCATGGCC GTTGTCTGTCG CCGCCGCGGC TCCCGGGGCT
51  GGATGGGGGG CCGAGGCCAG CCAGTGGCAC CCGGAAGAAA GAGACGCGGC
101 GCGGCGGACG CCGACACCCT CAGGACGAGT GTCCGGACTT GCCCACAGCC
151 TCAAGGAGGA GACGGCGAGG CCGGCCCCCC GCTGTCCCTG GTGTAAAGAA
201 GTCGCCGTAG CCGTCGCGGC CGGGACTCCC CGGGCTCTCG CCCTTCAGGT
251 TTCGTTGACA CTCAGGACCG TACGTACGCT GCGCCATGTT CAAGAACTG
301 AAGCAAAAGA TCAGCGAGGA GCAGCAGCAG CTCCAGCAGG CGCTGGCTCC
351 TGCTCAGGCG TCCTCCAATT CTTCAACACC AACAAAGATG AGGAGCAGGA
401 CATCTTCATT TACAGAGCAA CTTGATGAAG GTACACCCAA TAGAGAGTCA
451 GGTGACACAC AGTCTTTTGC ACAGAAGCTC CAGCTCCGGG TGCCCTCCGT
501 GGAGTCTTTG TTTCTGAAGTC CGATAAAGGA ATCTCTATTC CGGTCTTCTT
551 CTAAAGAGTC TTTGGTACGA ACATCTTCCA GAGAATCCCT GAATCGACTT
601 GACCTGGACA GTTCTACTGC CAGTTTTGAT CCACCCTCTG ATATGGATAG
651 CGAGGCTGAA GACTTGGTAG GGAATTCAGA CAGTCTCAAC AAAGAACAGT
701 TGATTCAGCG GTTGCGAAGA ATGGAACGAA GCTTAAGTAG CTACAGGGGA
751 AAATATTCTG AGCTTGTTAC AGCTTATCAG ATGCTTCAGA GAGAGAAGAA
801 AAAGCTACAA GGTATATTAA GTCAGAGTCA GGATAAATCA CTTCTGGAGAA
851 TAGCAGAATT AAGAGAGGAG CTCCAAATGG ACCAGCAGGC AAAGAAACAT
901 CTGCAAGAGG AGTTTGATGC ATCTTTAGAG GAGAAAGATC AGTATATCAG
951 TGTTCTCCAA ACTCAGGTTT CTCTACTGAA ACAACGATTA CGAAATGGCC
1001 CGATGAATGT TGATGTACTG AAACCACTTC CTCAGCTGGA ACCACAGGCT
1051 GAAGTCTTCA CTAAAGAAGA GAATCCAGAA AGTGATGGAG AGCCAGTAGT
1101 GGAAGATGGA ACTTCTGTAA AAACACTGGA AACACTCCAG CAAAGAGTGA
1151 AGCGTCAAGA GAACCTACTT AAGCGTTGTA AGGAAACAAT TCAGTCACAT
1201 AAGGAACAAT GTACACTATT AACTAGTGAA AAAGAAGCTC TGCAAGAACA
1251 ACTGGATGAA AGACTTCAAG AACTAGAAAA GATAAAGGAC CTTCATATGG
1301 CCGAGAAGAC TAAACTTATC ACTCAGTTGC GTGATGCAAA GAACTTAATT
1351 GAACAGCTTG AACAAGATAA GGGAATGGTA ATCGCAGAGA CAAAACGTCA
1401 GATGCATGAA ACCCTGGAAA TGAAAAGAAGA AGAAATTGCT CAACTCCGTA
1451 GTCGCATCAA ACAGATGACT ACCCAGGGAG AGGAATTACG GGAACAGAAA
1501 GAAAAGTCCG AAAGAGCTGC TTTTGAGGAA CTTGAAAAAG CTTTGAGTAC
1551 AGCCCAAAAA ACAGAGGAAG CACGGAGAAA ACTGAAGGCA GAAATGGATG
1601 AACAAATAAA AACTATCGAA AAAACAAGTG AGGAGGAACG CATCAGTCTT
1651 CAACAGGAAT TAAGTCGGGT GAAACAGGAG GTTGTGTATG TAATGAAAAA
1701 ATCCTCAGAA GAACAAATTG CTAAGCTACA GAAGCTTCAT GAAAAGGAGC
1751 TGGCCAGAAA AGAGCAGGAA CTGACCAAGA AGCTTCAGAC CCGAGAAAGG
1801 GAATTTTCAGG AACAAATGAA AGTAGCTCTT GAAAAGAGTC AATCAGAATA
1851 TTTGAAGATC AGCCAAGAAA AAGAACAGCA AGAATCTTTG GCCCTAGAAG
1901 AGTTAGAGTT GCAGAAAAAA GCAATCCTCA CAGAAAGTGA AAATAAACTT
1951 CGGGACCTTC AGCAAGAAGC AGAGACTTAC AGAACTAGAA TTCTGAATT
2001 GGAAAGTTCT TTGGAAAAAA GCTTACAAGA AAACAAAAT CAGTCAAAAG
2051 ATTTGGCTGT TCATCTGGAA GCTGAAAAAA ATAAGCACAA TAAGGAGATT
2101 ACAGTCATGG TTGAAAAACA CAAGACAGAA TTGGAAAGCC TTAAGCATCA
2151 GCAGGATGCC CTTTGGACTG AAAAAGCTCA AGTCTTAAAG CAACAATATC
2201 AGACTGAAAT GGAAAAACTT AGGGAAGAGT GTGAACAAGA AAAAGAAACA
2251 TTGTTGAAAG ACAAAGAGAT TATCTTCCAG GCCCACATAG AAGAAATGAA
2301 TGAAAAGACT TTAGAAAAGC TTGATGTGAA GCAAACAGAA CTAGAATCAT
2351 TATCTTCTGA ACTGTCAGAA GTATTAAAAG CCCGTCACAA ACTAGAAGAG
2401 GAACTTTCTG TTCTGAAAGA TCAAACAGAT AAAATGAAGC AGGAATTAGA
2451 GGCCAAGATG GATGAACAGA AAAATCATCA CCAGCAGCAA GTTGACAGTA

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2501	TCATTAAAGA	ACACGAGGTA	TCTATCCAGA	GGACTGAGAA	GGCATTAATA
2551	GATCAAATTA	ATCAACTTGA	GCTTCTCTTG	AAGGAAAGGG	ACAAGCATTT
2601	GAAAGAGCAT	CAGGCTCATG	TAGAAAATTT	AGAGGCAGAT	ATTAAAAGGT
2651	CTGAAGGGGA	ACTCCAGCAG	GCATCTGCTA	AGCTGGACGT	TTTTCAGTCT
2701	TACCAGAGTG	CCACACATGA	GCAGACAAAA	GCATATGAGG	AACAGTTGGC
2751	CCAATTGCAG	CAGAAAGTTGT	TGGATTTGGA	AACAGAAAGA	ATTCTTCTTA
2801	CCAAACAGGT	TGCTGAAGTT	GAAGCACAAA	AGAAAGATGT	TTGTACTGAG
2851	TTAGATGCTC	ACAAAAATCCA	GGTGCAGGAC	TTAATGCAGC	AACTTGAAAA
2901	ACAAAAATAGT	GAAATGGAGC	AAAAAGTAAA	ATCTTTAACC	CAAGTCTATG
2951	AGTCCAAACT	TGAAGATGGT	AACAAAGAAC	AGGAACAGAC	AAAGCAAATC
3001	TTGGTGGAAA	AGGAAAATAT	GATTTTACAA	ATGAGAGAAG	GACAGAAGAA
3051	AGAAATTGAG	ATACTCACAC	AGAAATTGTC	AGCCAAGGAG	GACAGTATTC
3101	ATATTTTGAA	TGAGGAATAT	GAAACCAAAT	TTAAAAACCA	AGAAAAAAG
3151	ATGGAAAAAG	TTAAGCAGAA	AGCAAAGGAG	ATGCAAGAAA	CGTTAAAGAA
3201	AAAATTACTG	GATCAGGAAG	CCAAACTTAA	GAAAGAGCTT	GAAAATACTG
3251	CTCTAGAGCT	TAGTCAGAAA	GAAAAACAGT	TTAATGCCAA	AATGCTGGAA
3301	ATGGCACAGG	CTAACTCAGC	TGGAATCAGT	GATGCAGTGT	CAAGACTGGA
3351	AACAAACCAA	AAAGAACAAA	TAGAAAGTCT	TACTGAGGTT	CATCGACGAG
3401	AACTCAATGA	TGTCATATCA	ATCTGGGAAA	AGAAACTTAA	TCAGCAAGCT
3451	GAAGAACTTC	AGGAAATACA	TGAAATCCAA	TTACAGGAAA	AAGAACAAGA
3501	GGTAGCAGAA	CTGAAACAAA	AGATCCTCCT	ATTTGGGTGT	GAAAAAGAAG
3551	AGATGAACAA	GGAAATAACA	TGGCTGAAGG	AAGAAGGTGT	TAAGCAGGAT
3601	ACAACATTAA	ATGAATTACA	GGAACAGTTA	AAGCAGAAGT	CTGCCCATGT
3651	GAATTCTCTT	GCACAAGATG	AAACTAAACT	GAAAGCTCAT	CTTGAAAAGC
3701	TAGAGGTTGA	CTTGAATAAG	TCTCTGAAGG	AAAATACTTT	TCTTCAAGAG
3751	CAGCTAGTTG	AACTGAAGAT	GCTGGCAGAA	GAAGATAAGC	GGAAGGTTTC
3801	TGAGTTGACT	AGCAAGTTGA	AAACCACAGA	TGAAGAATTC	CAGAGTTTGA
3851	AATCTTCACA	TGAAAAAAGT	AACAAAAGCC	TAGAGGACAA	GAGCTTGGA
3901	TTTAAAAAAC	TGTCTGAGGA	ACTAGCGATT	CAGCTAGATA	TTTGCTGTAA
3951	GAAAACCGAA	GCCTTATTAG	AAGCTAAAAC	AAATGAGCTA	ATCAACATTA
4001	GTAGTAGTAA	AACTAATGCC	ATTCTTTCTA	GGATTTCTCA	TTGTCAGCAC
4051	CGTACAACCTA	AAGTTAAGGA	GGCACTGTTA	ATTAAAACTT	GCACAGTTTC
4101	TGAATTAGAA	GCACAACCTA	GACAGTTGAC	AGAGGAGCAA	AATACACTAA
4151	ATATTTCTTT	TCAACAGGCT	ACTCATCAGT	TAGAAGAAAA	AGAAAATCAA
4201	ATTAAGAGCA	TGAAGGCTGA	TATTGAAAGT	CTTGTAACAG	AAAAAGAAGC
4251	CTTACAGAAG	GAAGGAGGCA	ATCAGCAACA	GGCTGCTTCT	GAAAAGGAGT
4301	CTTGTATAAC	ACAGTTGAAG	AAAGAGTTAT	CTGAAAACAT	CAATGCTGTC
4351	ACATTGATGA	AAGAAGAGCT	TAAAGAAAAA	AAAGTTGAGA	TTAGCAGTCT
4401	TAGTAAACAA	CTAACTGATT	TGAATGTTCA	GCTTCAAAAT	AGCATCAGCC
4451	TATCCGAAAA	AGAAGCAGCC	ATTTTCATCAC	TAAGAAAGCA	GTATGATGAA
4501	GAAAAATGTG	AATTGCTGGA	TCAGGTGCAA	GATTTATCTT	TTAAAGTTGA
4551	CACTCTGAGT	AAAGAGAAAA	TTTCTGCTCT	TGAGCAGGTA	GATGACTGGT
4601	CCAATAAATT	CTCAGAATGG	AAGAAGAAAG	CACAGTCAAG	ATTTACACAG
4651	CATCAAAACA	CTGTTAAAGA	ATTGCAGATC	CAGCTTGAGT	TAAAATCAAA
4701	GGAAGCTTAT	GAAAAGGATG	AGCAGATAAA	TTTATTGAAG	GAAGAGCTTG
4751	ATCAGCAAAA	TAAAAGATTT	GATTGTTTAA	AGGGTGAAAT	GGAAGACGAC
4801	AAGAGCAAGA	TGGAGAAAAA	GGAGTCTAAT	TTAGAAACAG	AGTTAAAGTC
4851	TCAAACAGCA	AGAATTATGG	AATTAGAGGA	CCATATTACC	CAGAAAACCTA
4901	TTGAAATAGA	GTCCTTAAAT	GAAGTCTTAA	AAAATTACAA	TCAACAAAAG
4951	GATATTGAAC	ACAAAGAATT	GGTTCAGAAA	CTTCAACATT	TTCAAGAGTT
5001	AGGAGAAGAA	AAGGACAACA	GGGTAAAGA	AGCTGAAGAA	AAAATCTTAA
5051	CACCTGAAAA	CCAAGTTTAT	TCCATGAAAG	CTGAACTTGA	AACTAAGAAG
5101	AAAGAATTAG	AACATGTGAA	TTTAAGTGTG	AAAAGCAAAG	AGGAGGAGTT
5151	AAAGGCATTG	GAAGATAGGC	TTGAGTCAGA	AAGTGCTGCA	AAATTAGCAG
5201	AGTTGAAGAG	AAAAGCTGAA	CAAAAAATTG	CTGCCATTAA	GAAGCAGTTG

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5251	TTATCTCAAA	TGGAAGAGAA	AGAAGAACAG	TATAAAAAAG	GTACAGAAAG
5301	CCATTTGAGT	GAGCTAAATA	CAAAATTGCA	GGAAAGAGAA	AGGGAAGTTC
5351	ACATCTTGGA	AGAAAACTT	AAGTCAGTGG	AAAGTTCACA	GTCAGAAACA
5401	TTAATTGTAC	CCAGATCAGC	AAAAAATGTG	GCAGCATATA	CTGAACAAGA
5451	AGAAGCAGAT	TCCCAAGGCT	GTGTGCAGAA	GACATATGAA	GAAAAAATCA
5501	GTGTTTTTACA	AAGAACTTA	ACTGAAAAAG	AAAAGCTATT	GCAGAGGGTA
5551	GGGCAGGAAA	AAGAAGAGAC	AGTTTCTTCT	CATTTTGAAA	TGCGATGCCA
5601	ATACCAGGAG	CGCTTAATAA	AGCTAGAACA	TGCTGAGGCA	AAGCAACATG
5651	AAGATCAAAG	TATGATAGGT	CATCTTCAAG	AGGAGCTTGA	AGAAAAAAC
5701	AAGAAATATT	CCTTGATAGT	AGCCCAGCAT	GTGGAAAAAG	AAGGAGGTAA
5751	AAATAACATA	CAGGCAAAGC	AAACTTGGA	AAATGTGTTT	GACGACGTCC
5801	AGAAAACCCT	CCAGGAGAAG	GAACATAACC	GTCAGATTTT	GGAGCAAAAG
5851	ATAAAAGAGC	TGGATTCCCTG	CTTAGTAAGA	CAGAAAGAAG	TACATAGAGT
5901	TGAAATGGAA	GAGTTGACCT	CAAAATATGA	AAAATTACAG	GCTTTACAAC
5951	AGATGGATGG	AAGAAATAAA	CCCACAGAAC	TTTTTGGAAGA	AAACACTGAA
6001	GAAAAGTCCA	AATCACATTT	GGTCCAACCC	AAATTGCTTA	GTAACATGGA
6051	AGCCCAGCAC	AATGATCTGG	AGTTTAAATT	AGCCGGGGCA	GAACGGGAGA
6101	AACAGAACT	GGGCAAGGAG	ATTGTTAGAT	TGCAGAAAGA	CCTTCGAATG
6151	TTGAGAAAGG	AGCATCAGCA	AGAATTGGAA	ATACTAAAGA	AAGAATATGA
6201	TCAAGAAAGG	GAAGAGAAAA	TCAAACAGGA	GCAGGAAGAT	CTTGAAGTGA
6251	AGCACAATTC	CACATTAAAA	CAGCTGATGA	GGGAGTTTAA	TACACAGCTG
6301	GCACAAAAGG	AACAAGAGCT	GGAAATGACC	ATAAAAGAAA	CTATCAATAA
6351	GGCCCAGGAG	GTGGAGGCTG	AACTTTTAGA	AAGCCATCAA	GAAGAGACAA
6401	ATCAGTTACT	TAAAAAATT	GCTGAGAAAG	ATGATGATCT	AAAACGAACA
6451	GCCAAAAGAT	ATGAAGAAAT	CCTTGATGCT	CGTGAAGAAG	AAATGACTGC
6501	AAAAGTAAGG	GACCTGCAGA	CTCAACTTGA	GGAGCTGCAG	AAGAAATACC
6551	AGCAAAAGCT	AGAGCAGGAG	GAGAACCCTG	GCAATGATAA	TGTAACAATT
6601	ATGGAGCTAC	AGACACAGCT	AGCACAGAAG	ACGACTTTAA	TCAGTGATTC
6651	GAAATTGAAA	GAGCAAGAGT	TCAGAGAACA	GATTCACAAT	TTAGAAGACC
6701	GTTTGAAGAA	ATATGAAAAG	AATGTATATG	CAACAACGTG	GGGGACACCT
6751	TACAAAGGTG	GCAATTTGTA	CCATACGGAT	GTCTCACTCT	TTGGAGAACC
6801	TACCGAATTT	GAGTATTTGC	GAAAAAGTGCT	TTTTGAGTAT	ATGATGGGTC
6851	GTGAGACTAA	GACCATGGCA	AAAGTTATAA	CCACCGTACT	GAAGTTCCCT
6901	GATGATCAGA	CTCAGAAAAT	TTTGGAAGA	GAAGATGCTC	GGCTGATGTC
6951	ATGGCTCCGA	TCTTCATCTT	GAAGAAGAGT	GACATTGGGT	GACTGCTGCT
7001	TGGAAAACCTG	TCCACACTTG	CTACTCTTTG	AGAATGAAGT	TGTCATTCAG
7051	GGCCCCTCAT	GTAGCCAAAA	GACCAAGAAA	AATCTGGCCC	ACAGATAAGT
7101	TGCAGACTGC	CTTTAAAATA	GATTTTATCA	GTGGAGAAAT	GGTGATAGTT
7151	TTTTCTTCAG	TTTTCTCTTG	GGAAGAGTTT	TATGTTGTTT	AAAAGATATT
7201	TTGATAACTT	AACCTGCTTT	ATGGGCTTAC	ATAATATTCC	TTTCATCCAT
7251	TCTTTTTTAAA	GAACGGCTTA	CCTTTCCTAT	TTATTTTTTAG	GGTGATTTTT
7301	TAAAAAGACT	TGTGCAATAC	ATTTTGAGGT	GAACTTAGT	GGATTTTTTC
7351	TGATAAATTA	GAGCATTTAA	TTGACTATTT	TATTCAGGTT	GATCTGTTGA
7401	ATATTTGCTA	AAGACCAGTT	CTTTAAGCTA	AGACATGTAA	AAAATCCCAA
7451	ATGGCAGTAC	CTCATTGTTT	ACTTAGCTTT	TGTACTTATA	TTTTTCAGAG
7501	GAAAAACAC	TACTGTAAAT	TGTGAATAGC	CAATACATAA	CTGTATTGTA
7551	TGCAAATCTG	TGATTGTTGG	CAGTGTCATC	TCTGAGAAAC	AGATAAATAA
7601	AGTTTATTTA	CTATATAACC	AAAAAAAAAA	AAAAAA	

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Fig. 7: SEQ ID NO. 4: amino acid sequence of human golgin-245, splice variant 2 (GenBank accession number Q13439)

Length: 2230 aa

1	MFKKLKQKIS	EEQQQLQQAL	APAQASSNSS	TPTRMRSRTS	SFTEQLDEGT
51	PNRESGDTQS	FAQKLQLRVP	SVESLFRSPI	KESLFRSSSK	ESLVRTSSRE
101	SLNRLDLDS	TASFDPPSDM	DSEAEDLVGN	SDSLNKEQLI	QRLRRMERSL
151	SSYRGKYSEL	VTAYQMLQRE	KKKLQGILSQ	SQDKSLRRIA	ELREELQMDQ
201	QAKKHLQEEF	DASLEEKDQY	ISVLQTQVSL	LKQRLRNGPM	NVDVLKPLPQ
251	LEPQAEVFTK	EENPESDGEP	VVEDGTSVKT	LETLQQRVVK	QENLLKRCKE
301	TIQSHKEQCT	LLTSEKEALQ	EQLDERLQEL	EKIKDLHMAE	KTKLITQLRD
351	AKNLIEQLEQ	DKGMVIAETK	RQMHELTLEMK	EEEIAQLRSR	IKQMTTQGEE
401	LREQKEKSER	AAFEELEKAL	STAQKTEEAR	RKLKAEMDEQ	IKTIEKTSEE
451	ERISLQQELS	RVKQEVVDVM	KKSSEEQIAK	LQKLHEKELA	RKEQELTKKL
501	QTREREFQEQ	MKVALEKSQS	EYLKISQKEE	QQESLAL EEL	ELQKKAILTE
551	SENKLRDLQQ	EAETYRTRIL	ELESSLEKSL	QENKNQSKDL	AVHLEAEKNK
601	HNKEITVMVE	KHKTELES LK	HQQDALWTEK	LQVLKQQYQT	EMEKLREKCE
651	QEKETLLKDK	EIIFQAHIEE	MNEKTLEKLD	VKQTELESLS	SELSEVLKAR
701	HKLEELSVL	KDQTDKMKQE	LEAKMDEQKN	HHQQQVDSII	KEHEVSIQRT
751	EKALKDQINQ	LELLLLKERDK	HLKEHQAHVE	NLEADIKRSE	GELQQASAKL
801	DVFQSYQSAT	HEQTKAYEEQ	LAQLQOKLLD	LETERILLTK	QVAEVEAQKK
851	DVCTELDAHK	IQVQDLMQQL	EKQNSEMEQK	VKSLTQVYES	KLEDGNKEQE
901	QTKQILVEKE	NMILQMREGQ	KKEIEILTQK	LSAKEDSIHI	LNEEYETKFK
951	NQEKKMEKVK	QKAKEMQETL	KKKLLDQEAK	LKKELENTAL	ELSQKEKQFN
1001	AKMLEMAQAN	SAGISDAVSR	LETNQKEQIE	SLTEVHRREL	NDVISIWEKK
1051	LNQQAEELQE	IHEIQLQEKE	QEV AELKQKI	LLFGCEKEEM	NKEITWLKEE
1101	GVKQD TTLNE	LQEQLKQKSA	HVNSLAQDET	KLKAHLEKLE	VDLNKSLKEN
1151	TFLQEQLVEL	KMLAEEDK RK	VSELTSKLKT	TDEEFQSLKS	SHEKSNKSLE
1201	DKSLEFKKLS	EELAIQLDIC	CKKTEALLEA	KTNELINISS	SKTNAILSRI
1251	SHCQHRTTKV	KEALLIKTCT	VSELEAQLRQ	LTEEQNTLNI	SFQQATHQLE
1301	EKENQIKSMK	ADIESLVTEK	EALQKEGGNQ	QQAASEKESC	ITQLKKELSE
1351	NINAVTLMKE	ELKEKKVEIS	SLSKQLTDLN	VQLQNSISLS	EKEAAISSLR
1401	KQYDEEKCEL	LDQVQDLSFK	VDTLSKEKIS	ALEQVDDWSN	KFSEWKKAQ
1451	SRFTQHONTV	KELQIQLELK	SKEAYEKDEQ	INLLKEELDQ	QNKRFDC LKG
1501	EMEDDKSKME	KKESNLETEL	KSQTARIMEL	EDHITQKTIE	IESLNEVLKN
1551	YNQQKDIEHK	ELVQKLQHFQ	ELGEEKDNRV	KEAEKILTTL	ENQVYSMAE
1601	LETKKKELEH	VNLSVKSKEE	ELKALEDRL E	SESAAKLAEL	KRKAEQKIAA
1651	IKKQLLSQME	EKEEQYKKGT	ESHLSELNTK	LQEREREVHI	LEEKLSVES
1701	SQSETLIVPR	SAKNVAAYTE	QEEADSQGCV	QKTYEEKISV	LQRNLTEKEK
1751	LLQRVGQEKE	ETVSSH FEMR	CQYQERLIKL	EHAEAKQHED	QSMIGHLQEE
1801	LEEKNNKYSL	IVAQHVEKEG	GKNNIQAKQN	LENVFDDVQK	TLQEKELTCQ
1851	ILEQKIKELD	SCLVRQKEVH	RVEMEELTSK	YEKLQALQQM	DGRNKPTELL
1901	EENTEEKSKS	HLVQPKLLSN	MEAQHNDLEF	KLAGAEREKQ	KLKGEIVRLQ
1951	KDLRMLRKEH	QQELEILKKE	YDQEREKIK	QEQedLELKH	NSTLQQLMRE
2001	FNTQLAQKEQ	ELEMTIKETI	NKAQEV E AEL	LESHQEETNQ	LLKKIAEKDD
2051	DLKRTAKRYE	EILDAREEEM	TAKVRDLQTO	LEELQKKYQQ	KLEQ EENPGN
2101	DNVTIMELQT	QLAQKTT LIS	DSKLKEQEFR	EQIHNLEDRL	KKY EKNVYAT
2151	TVGTPYKGGN	LYHTDVSLFG	EPTEFEYLRK	VLFEYMMGRE	TKTMAKVITT
2201	VLKFPDDQTQ	KILEREDARL	MFTSPRSGIF		

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Fig. 8: SEQ ID NO. 5: nucleotide sequence of human golgin-245 cDNA, splice variant 2 (GenBank accession number U41740)

Length: 7695 bp

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1   GCAACGAAGG TACCATGGCC GTTGTCTGTCG CCGCCGCGGC TCCCGGGGCT
51  GGATGGGGGG CCGAGGCCAG CCAGTGGCAC CCGGAAGAAA GAGACGCGGC
101 GGCGGCGACG CCGACACCCT CAGGACGAGT GTCCGGACTT GCCCAGAGCC
151 TCAAGGAGGA GACGGCGAGG CCCGCCCCCC GCTGTCCCTG GTGTAAAGAA
201 GTCGCCGTAG CCGTCGCGGC CGGGACTCCC CGGGCTCTCG CCCTTCAGGT
251 TTCGTTGACA CTCAGGACCG TACGTACGCT GCGCCATGTT CAAGAAACTG
301 AAGCAAAAGA TCAGCGAGGA GCAGCAGCAG CTCCAGCAGG CGCTGGGCTCC
351 TGCTCAGGCG TCCTCCAATT CTTCAACACC AACAAGAAATG AGGAGCAGGA
401 CATCTTCATT TACAGAGCAA CTTGATGAAG GTACACCCAA TAGAGAGTCA
451 GGTGACACAC AGTCTTTTGC ACAGAAGCTC CAGCTCCGGG TGCCCTCCGT
501 GGAGTCTTTG TTTCGAAGTC CGATAAAGGA ATCTCTATTC CGGTCTTCTT
551 CTAAAGAGTC TTTGGTACGA ACATCTTCCA GAGAATCCCT GAATCGACTT
601 GACCTGGACA GTTCTACTGC CAGTTTTGAT CCACCCTCTG ATATGGATAG
651 CGAGGCTGAA GACTTGGTAG GGAATTCAGA CAGTCTCAAC AAAGAACAGT
701 TGATTCAGCG GTTGCGAAGA ATGGAACGAA GCTTAAGTAG CTACAGGGGA
751 AAATATTCTG AGCTTGTTAC AGCTTATCAG ATGCTTCAGA GAGAGAAGAA
801 AAAGCTACAA GGTATATTAA GTCAGAGTCA GGATAAATCA CTCGGAGAA
851 TAGCAGAAAT AAGAGAGGAG CTCCAAATGG ACCAGCAGGC AAAGAAACAT
901 CTGCAAGAGG AGTTTGATGC ATCTTTAGAG GAGAAAGATC AGTATATCAG
951 TGTTCTCCAA ACTCAGGTTT CTCTACTGAA ACAACGATTA CGAAATGGCC
1001 CGATGAATGT TGATGTACTG AAACCACTTC CTCAGCTGGA ACCACAGGCT
1051 GAAGTCTTCA CTAAAGAAGA GAATCCAGAA AGTGATGGAG AGCCAGTAGT
1101 GGAAGATGGA ACTTCTGTAA AAACACTGGA AACACTCCAG CAAAGAGTGA
1151 AGCGTCAAGA GAACCTACTT AAGCGTTGTA AGGAAACAAT TCAGTCACAT
1201 AAGGAACAAT GTACACTATT AACTAGTGAA AAAGAAGCTC TGCAAGAACA
1251 ACTGGATGAA AGACTTCAAG AACTAGAAAA GATAAAGGAC CTTCATATGG
1301 CCGAGAAGAC TAAACTTATC ACTCAGTTGC GTGATGCAAA GAACTTAATT
1351 GAACAGCTTG AACAAGATAA GGAATGGTA ATCGCAGAGA CAAAACGTCA
1401 GATGCATGAA ACCCTGGAAA TGAAAGAAGA AGAAATTGCT CAACTCCGTA
1451 GTCGCATCAA ACAGATGACT ACCCAGGGAG AGGAATTACG GGAACAGAAA
1501 GAAAAGTCCG AAAGAGCTGC TTTTGAGGAA CTTGAAAAAG CTTTGAGTAC
1551 AGCCCAAAAA ACAGAGGAAG CACGGAGAAA ACTGAAGGCA GAAATGGATG
1601 AACAAATAAA AACTATCGAA AAAACAAGTG AGGAGGAACG CATCAGTCTT
1651 CAACAGGAAT TAAGTCGGGT GAAACAGGAG GTTGTTGATG TAATGAAAAA
1701 ATCCTCAGAA GAACAAATTG CTAAGCTACA GAAGCTTCAT GAAAAGGAGC
1751 TGGCCAGAAA AGAGCAGGAA CTGACCAAGA AGCTTCAGAC CCGAGAAAGG
1801 GAATTCAGAG AACAAATGAA AGTAGCTCTT GAAAAGAGTC AATCAGAATA
1851 TTTGAAGATC AGCCAAGAAA AAGAACAGCA AGAATCTTTG GCCCTAGAAG
1901 AGTTAGAGTT GCAGAAAAAA GCAATCCTCA CAGAAAGTGA AAATAAACTT
1951 CGGGACCTTC AGCAAGAAGC AGAGACTTAC AGAACTAGAA TTCTTGAATT
2001 GGAAAGTTCT TTGGAAAAAA GCTTACAAGA AAACAAAAAT CAGTCAAAAG
2051 ATTTGGCTGT TCATCTGGAA GCTGAAAAAA ATAAGCACAA TAAGGAGATT
2101 ACAGTCATGG TTGAAAAACA CAAGACAGAA TTGGAAAGCC TTAAGCATCA
2151 GCAGGATGCC CTTTGGACTG AAAAATCCA AGTCTTAAAG CAACAATATC
2201 AGACTGAAAT GGAAAACTT AGGGAAAAGT GTGAACAAGA AAAAGAAACA
2251 TTGTTGAAAG ACAAAGAGAT TATCTTCCAG GCCCACATAG AAGAAATGAA
2301 TGAAAAGACT TTAGAAAAGC TTGATGTGAA GCAAACAGAA CTAGAATCAT
2351 TATCTTCTGA ACTGTCAGAA GTATTAAAAG CCCGTCACAA ACTAGAAGAG
2401 GAACTTTCTG TTCTGAAAGA TCAAACAGAT AAAATGAAGC AGGAATTAGA
2451 GGCCAAGATG GATGAACAGA AAAATCATCA CCAGCAGCAA GTTGACAGTA
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2501	TCATTAAAGA	ACACGAGGTA	TCTATCCAGA	GGACTGAGAA	GGCATTAAAA
2551	GATCAAATTA	ATCAACTTGA	GCTTCTCTTG	AAGGAAAGGG	ACAAGCATTT
2601	GAAAGAGCAT	CAGGCTCATG	TAGAAAATTT	AGAGGCAGAT	ATTAAGAGGT
2651	CTGAAGGGGA	ACTCCAGCAG	GCATCTGCTA	AGCTGGACGT	TTTTCAGTCT
2701	TACCAGAGTG	CCACACATGA	GCAGACAAAA	GCATATGAGG	AACAGTTGGC
2751	CCAATTGCAG	CAGAAAGTTGT	TGGATTTGGA	AACAGAAAGA	ATTCTTCTTA
2801	CCAAACAGGT	TGCTGAAGTT	GAAGCACAAA	AGAAAGATGT	TTGTACTGAG
2851	TTAGATGCTC	ACAAAATCCA	GGTGCAGGAC	TTAATGCAGC	AACTTGAAAA
2901	ACAAAATAGT	GAAATGGAGC	AAAAAGTAAA	ATCTTTAACC	CAAGTCTATG
2951	AGTCCAAACT	TGAAGATGGT	AACAAAGAAC	AGGAACAGAC	AAAGCAAATC
3001	TTGGTGGAAA	AGGAAAATAT	GATTTTACAA	ATGAGAGAAG	GACAGAAGAA
3051	AGAAATTGAG	ATACTCACAC	AGAAATTGTC	AGCCAAGGAG	GACAGTATTC
3101	ATATTTTGAA	TGAGGAATAT	GAAACCAAAT	TTAAAAACCA	AGAAAAAAG
3151	ATGGAAAAAG	TTAAGCAGAA	AGCAAAGGAG	ATGCAAGAAA	CGTTAAAGAA
3201	AAAATTACTG	GATCAGGAAG	CCAACTTAA	GAAAGAGCTT	GAAAATACTG
3251	CTCTAGAGCT	TAGTCAGAAA	GAAAAACAGT	TTAATGCCAA	AATGCTGGAA
3301	ATGGCACAGG	CTAACTCAGC	TGGAATCAGT	GATGCAGTGT	CAAGACTGGA
3351	AACAAACCAA	AAAGAACAAA	TAGAAAGTCT	TACTGAGGTT	CATCGACGAG
3401	AACTCAATGA	TGTCATATCA	ATCTGGGAAA	AGAAACTTAA	TCAGCAAGCT
3451	GAAGAACTTC	AGGAAATACA	TGAAATCCAA	TTACAGGAAA	AAGAACAAGA
3501	GGTAGCAGAA	CTGAAACAAA	AGATCCTCCT	ATTTGGGTGT	GAAAAAGAAG
3551	AGATGAACAA	GGAAATAACA	TGGCTGAAGG	AAGAAGGTGT	TAAGCAGGAT
3601	ACAACATTAA	ATGAATTACA	GGAACAGTTA	AAGCAGAAGT	CTGCCCATGT
3651	GAATTCTCTT	GCACAAGATG	AAACTAAACT	GAAAGCTCAT	CTTGAAAAGC
3701	TAGAGGTTGA	CTTGAATAAG	TCTCTGAAGG	AAAATACTTT	TCTTCAAGAG
3751	CAGCTAGTTG	AACTGAAGAT	GCTGGCAGAA	GAAGATAAGC	GGAAGGTTTC
3801	TGAGTTGACT	AGCAAGTTGA	AAACCACAGA	TGAAGAATTC	CAGAGTTTGA
3851	AATCTTCACA	TGAAAAAAGT	AACAAAAGCC	TAGAGGACAA	GAGCTTGGAA
3901	TTTAAAAAAC	TGTCTGAGGA	ACTAGCGATT	CAGCTAGATA	TTTGCTGTAA
3951	GAAAACCGAA	GCCTTATTAG	AAGCTAAAAC	AAATGAGCTA	ATCAACATTA
4001	GTAGTAGTAA	AACTAATGCC	ATTCTTTCTA	GGATTTCTCA	TTGTCAGCAC
4051	CGTACAACCTA	AAGTTAAGGA	GGCACTGTTA	ATTAACACTT	GCACAGTTTC
4101	TGAATTAGAA	GCACAACCTA	GACAGTTGAC	AGAGGAGCAA	AATACACTAA
4151	ATATTTCTTT	TCAACAGGCT	ACTCATCAGT	TAGAAGAAAA	AGAAAATCAA
4201	ATTAAGAGCA	TGAAGGCTGA	TATTGAAAGT	CTTGTAACAG	AAAAAGAAGC
4251	CTTACAGAAG	GAAGGAGGCA	ATCAGCAACA	GGCTGCTTCT	GAAAAGGAGT
4301	CTTGTATAAC	ACAGTTGAAG	AAAGAGTTAT	CTGAAAACAT	CAATGCTGTC
4351	ACATTGATGA	AAGAAGAGCT	TAAAGAAAAA	AAAGTTGAGA	TTAGCAGTCT
4401	TAGTAAACAA	CTAACTGATT	TGAATGTTCA	GCTTCAAAT	AGCATCAGCC
4451	TATCCGAAAA	AGAAGCAGCC	ATTCATCAC	TAAGAAAGCA	GTATGATGAA
4501	GAAAAATGTG	AATTGCTGGA	TCAGGTGCAA	GATTTATCTT	TTAAAGTTGA
4551	CACTCTGAGT	AAAGAGAAAA	TTTCTGCTCT	TGAGCAGGTA	GATGACTGGT
4601	CCAATAAATT	CTCAGAATGG	AAGAAGAAAG	CACAGTCAAG	ATTTACACAG
4651	CATCAAAACA	CTGTTAAAGA	ATTGCAGATC	CAGCTTGAGT	TAAAATCAAA
4701	GGAAAGCTTAT	GAAAAGGATG	AGCAGATAAA	TTTATTGAAG	GAAGAGCTTG
4751	ATCAGCAAAA	TAAAAGATTT	GATTGTTTAA	AGGGTGAAAT	GGAAAGACGAC
4801	AAGAGCAAGA	TGGAGAAAAA	GGAGTCTAAT	TTAGAAACAG	AGTTAAAGTC
4851	TCAAACAGCA	AGAATTATGG	AATTAGAGGA	CCATATTACC	CAGAAAACCTA
4901	TTGAAATAGA	GTCCTTAAAT	GAAGTTCTTA	AAAATTACAA	TCAACAAAAG
4951	GATATTGAAC	ACAAAGAATT	GGTTCAGAAA	CTTCAACATT	TTCAAGAGTT
5001	AGGAGAAGAA	AAGGACAACA	GGGTAAAGA	AGCTGAAGAA	AAAATCTTAA
5051	CACTTGAAAA	CCAAGTTTAT	TCCATGAAAG	CTGAACTTGA	AACTAAGAAG
5101	AAAGAATTAG	AACATGTGAA	TTTAAGTGTG	AAAAGCAAAG	AGGAGGAGTT
5151	AAAGGCATTG	GAAGATAGGC	TTGAGTCAGA	AAGTGCTGCA	AAATTAGCAG

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5201 AGTTGAAGAG AAAAGCTGAA CAAAAAATTG CTGCCATTAA GAAGCAGTTG
5251 TTATCTCAAA TGGAAGAGAA AGAAGAACAG TATAAAAAAG GTACAGAAAG
5301 CCATTTGAGT GAGCTAAATA CAAAATTGCA GGAAAGAGAA AGGGAAGTTC
5351 ACATCTTGGA AGAAAAACTT AAGTCAGTGG AAAGTTCACA GTCAGAAACA
5401 TTAATTGTAC CCAGATCAGC AAAAAATGTG GCAGCATATA CTGAACAAGA
5451 AGAAGCAGAT TCCCAAGGCT GTGTGCAGAA GACATATGAA GAAAAAATCA
5501 GTGTTTTACA AAGAACTTA ACTGAAAAAG AAAAGCTATT GCAGAGGGTA
5551 GGGCAGGAAA AAGAAGAGAC AGTTTCTTCT CATTTTGAAA TGCGATGCCA
5601 ATACCAGGAG CGCTTAATAA AGCTAGAACA TGCTGAGGCA AAGCAACATG
5651 AAGATCAAAG TATGATAGGT CATCTTCAAG AGGAGCTTGA AGAAAAAAC
5701 AAGAAATATT CCTTGATAGT AGCCCAGCAT GTGGAAAAAG AAGGAGGTAA
5751 AAATAACATA CAGGCAAAGC AAAACTTGGA AAATGTGTTT GACGACGTCC
5801 AGAAAACCTT CCAGGAGAAG GAACTAACCT GTCAGATTTT GGAGCAAAAG
5851 ATAAAAGAGC TGGATTCTTG CTTAGTAAGA CAGAAAGAAG TACATAGAGT
5901 TGAAATGGAA GAGTTGACCT CAAAATATGA AAAATTACAG GCTTTACAAC
5951 AGATGGATGG AAGAAATAAA CCCACAGAAC TTTTGGAAGA AAACACTGAA
6001 GAAAAGTCCA AATCACATTT GGTCCAACCC AAATTGCTTA GTAACATGGA
6051 AGCCCAGCAC AATGATCTGG AGTTTAAATT AGCCGGGGCA GAACGGGAGA
6101 AACAGAAACT GGGCAAGGAG ATTGTTAGAT TGCAGAAAGA CCTTCGAATG
6151 TTGAGAAAGG AGCATCAGCA AGAATTGGAA ATACTAAAGA AAGAATATGA
6201 TCAAGAAAGG GAAGAGAAAA TCAAACAGGA GCAGGAAGAT CTTGAAGTGA
6251 AGCACAATTC CACATTAAAA CAGCTGATGA GGGAGTTTAA TACACAGCTG
6301 GCACAAAAGG AACAAAGAGT GGAATGACC ATAAAAGAAA CTATCAATAA
6351 GGCCCAGGAG GTGGAGGCTG AACTTTTAGA AAGCCATCAA GAAGAGACAA
6401 ATCAGTTACT TAAAAAATT GCTGAGAAAG ATGATGATCT AAAACGAACA
6451 GCCAAAAGAT ATGAAGAAAT CCTTGATGCT CGTGAAGAAG AAATGACTGC
6501 AAAAGTAAGG GACCTGCAGA CTCAACTTGA GGAGCTGCAG AAGAAATACC
6551 AGCAAAAGCT AGAGCAGGAG GAGAACCCTG GCAATGATAA TGTAACAATT
6601 ATGGAGCTAC AGACACAGCT AGCACAGAAG ACGACTTTAA TCAGTGATTC
6651 GAAATTGAAA GAGCAAGAGT TCAGAGAACA GATTCACAAT TTAGAAGACC
6701 GTTTGAAGAA ATATGAAAAG AATGTATATG CAACAACGTG GGGGACACCT
6751 TACAAAGGTG GCAATTTGTA CCATACGGAT GTCTCACTCT TTGGAGAACC
6801 TACCGAATTT GAGTATTTGC GAAAAGTGCT TTTTGAGTAT ATGATGGGTC
6851 GTGAGACTAA GACCATGGCA AAAGTTATAA CCACCGTACT GAAGTTCCCT
6901 GATGATCAGA CTCAGAAAAT TTTGGAAAGA GAAGATGCTC GGCTGATGTT
6951 TACTTCACCT CGCAGTGGTA TCTTCTGAGT AAACCATCAG TCTGTGCTTA
7001 GTTAACATGT GTCATGGCTC CGATCTTCAT CTTGAAGAAG AGTGACATTG
7051 GGTGACTGCT GCTTGAAAAA CTGTCCACAC TTGCTACTCT TTGAGAATGA
7101 AGTTGTCATT CAGGGCCCCT CATGTAGCCA AAAGACCAAG AAAAATCTGG
7151 CCCACAGATA AGTTGCAGAC TGCCTTTAAA ATAGATTTTA TCAGTGGAGA
7201 AATGGTGATA GTTTTTTCTT CAGTTTTCTC TTGGGAAGGA GTTTTATGTT
7251 GTTTAAAAGA TATTTTGATA ACTTAACCTG CTTTATGGGC TTACATAATA
7301 TTCCTTTCAT CCATTCTTTT TAAAGAACGG CTTACCTTTC CTATTTATTT
7351 TTAGGGTGAT TTTTTAAAAA GACTTGTGCA ATACATTTTG AGGTGAAACT
7401 TAGTGGATTT TTTCTGATAA ATTAGAGCAT TTAATTGACT ATTTTATTCA
7451 GGTTGATCTG TTGAATATTT GCTAAAGACC AGTTCTTTAA GCTAAGACAT
7501 GTAAAAAATC CCAAATGGCA GTACCTCATT GTTTACTTAG CTTTGTACT
7551 TATATTTTTT AGAGGAAAAA ACACTACTGT AAATTGTGAA TAGCCAATAC
7601 ATAAGTGTAT TGTATGAAA TCTGTGATTG TTGGCAGTGT CATCTCTGAG
7651 AAACAGATAA ATAAAGTTTA TTTACTATAA AAAAAAATAA AAAAG

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Fig. 9: SEQ ID NO. 6:amino acid sequence of human golgin-245, splice variant 3**Length: 2250 aa**

1	MFKKLKQKIS	EEQQQLQQAL	APAQASSNSS	TPTRMRSRTS	SFTEQLDEGT
51	PNRENASTHA	SKSPDSVNGS	EPSIPQSGDT	QSFAQKLQLR	VPSVESLFRS
101	PIKESLFRSS	SKESLVRTSS	RESLNRLDLD	SSTASFDPPS	DMDSEAEDLV
151	GNSDSLNEQ	LIQRLRRMER	SLSSYRGKYS	ELVTAYQMLQ	REKKKLQGIL
201	SQSQDKSLRR	IAELREELQM	DQQAKKHLQE	EFDASLEEKD	QYISVLQTQV
251	SLLKQRLRNG	PMNVDVLKPL	PQLEPQAEVF	TKEENPESDG	EPVVEDGTSV
301	KTLETLQQRV	KRQENLLKRC	KETIQSHKEQ	CTLLTSEKEA	LQEQLDERLQ
351	ELEKIKDLHM	AEKTKLITQL	RNAKNLIEQL	EQDKGMVIAE	TKRQMHETLE
401	MKEEEIAQLR	SRIKQMTTQG	EELREQKEKS	ERAAFEELK	ALSTAQKTEE
451	ARRKLKAEMD	EQIKTIEKTS	EEERISLQQE	LSRVKQEVVD	VMKKSSEEQI
501	AKLQKLHEKE	LARKEQELTK	KLQTREREFQ	EQMKVALEKS	QSEYLIKISQE
551	KEQQESLAL	ELELQKKAIL	TESENKLRLD	QQEAETYRTR	ILELESSLEK
601	SLQENKNQSK	DLAVHLEAEK	NKHNKEITVM	VEKHKTELES	LKHQQDALWT
651	EKLQVLKQQY	QTEMEKLREK	CEQEKETLLK	DKEIIFQAH	EEMNEKTLEK
701	LDVKQTELES	LSSELSEVLK	ARHKLEEEELS	VLKDQTDKMK	QELEAKMDEQ
751	KNHHQQQVDS	IIKEHEVSIQ	RTEKALKDQI	NQLELLLLKER	DKHLKEHQAH
801	VENLEADIKR	SEGELQQASA	KLDVFQSYQS	ATHEQTKAYE	EQLAQLQQKL
851	LDLETERILL	TKQVAEVEAQ	KKDVCTELDA	HKIQVQDLMQ	QLEKQNSEME
901	QKVKSLTQVY	ESKLEDGNKE	QEQTQKILVE	KENMILQMRE	GQKKEIEILT
951	QKLSAKEDSI	HILNEEYETK	FKNQEKMEK	VKQKAKEMQE	TLKKKLLDQE
1001	AKLKKELT	ALELSQKEKQ	FNAKMLEMAQ	ANSAGISDAV	SRLETNQKEQ
1051	IESLTEVHRR	ELNDVISIWE	KKLNQQAEEL	QEIHEIQLOE	KEQEVAEKQ
1101	KILLFGCEKE	EMNKEITWLK	EEGVKQDTTL	NELQEQLKQK	SAHVNSLAQD
1151	ETKLKAHLEK	LEVDLNKSLLK	ENTFLQEQLV	ELKMLAEEDK	RKVSELTSKL
1201	KTTDEEFQSL	KSSHEKSNKS	LEDKSLEFKK	LSEELAIQLD	ICCKKTEALL
1251	EAKTNELINI	SSSKTNAIIS	RISHCQHRTT	KVKEALLIKT	CTVSELEAQL
1301	RQLTEEQNTL	NISFQQATHQ	LEEKENQIKS	MKADIESLVT	EKEALQKEGG
1351	NQQQAASEKE	SCITQLKKEL	SENINAVTLM	KEELKEKKVE	ISSLSKQLTD
1401	LNVLQNSIS	LSEKEAAISS	LRKQYDEEKC	ELLDQVQDLS	FKVDTLSEK
1451	ISALEQVDDW	SNKFSEWKKK	AQSRFTQHQN	TVKELQIQLE	LKSKEAYEKD
1501	EQINLLKEEL	DQQNKRFDCL	KGEMEDDKSK	MEKKESNLET	ELKSQTARIM
1551	ELEDHITQKT	IEIESLNEVL	KNYNQQKDIE	HKELVQKLQH	FQELGEEKDN
1601	RVKEAEEKIL	TLENQVYSMK	ALETKKKKEL	EHVNLSVKSK	EEELKALEDR
1651	LESESAAKLA	ELKRKAEQKI	AAIKKQLLSQ	MEEKEEQYKK	GTESHLSELN
1701	TKLQEREREF	HILEEKLKSV	ESSQSETLIV	PRSAKNVAAY	TEQEEADSQG
1751	CVQKTYEEKI	SVLQRNLTEK	EKLLQVRGQE	KEETVSSHFE	MRCQYQERLI
1801	KLEHAEAKQH	EDQSMIGHLQ	EELEEKNKKY	SLIVAQHVEK	EGGKNNIQAK
1851	QNLENVFDDV	QKTLQEKELT	CQILEQKIKE	LDSCLVROKE	VHRVEMEELT
1901	SKYEKLQALQ	QMDGRNKPTE	LLEENTEEKS	KSHLVQPKLL	SNMEAQHNDL
1951	EFKLAGAERE	KQKLGKEIVR	LQKDLRMLRK	EHQQELEILK	KEYDQEREK
2001	IKQEEDLEL	KHNSTLQQLM	REFNTQLAQK	EQELEM TIKE	TINKAQEVEA
2051	ELLESHQEET	NQLLKKIAEK	DDDLKRTAKR	YEEILDAREE	EMTAKVRDLQ
2101	TQLEELQKKY	QQKLEQEENP	GNDNVTIMEL	QTQLAQKTTL	ISDSKLKEQE
2151	FREQIHNLED	RLKKYEKNVY	ATTVGTPYKG	GNLYHTDVSL	FGEPTFEFYL
2201	RKVLFEYMMG	RETKTMAKVI	TTVLKFPDDQ	TQKILEREDA	RLMSWLRS

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10/511096

Fig. 10: SEQ ID NO. 7: nucleotide sequence of human golgin-245 cDNA, splice variant 3**Length: 7743 bp**

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1   GCAACGAAGG TACCATGGCC GTTGTCGTCG CCGCCGCGGC TCCCGGGGCT
51  GGATGGGGGG CCGAGGCCAG CCAGTGGCAC CCGGAAGAAA GAGACGCGGC
101 GGCGGCGACG CCGACACCCT CAGGACGAGT GTCCGGACTT GCCCACAGCC
151 TCAAGGAGGA GACGGCGAGG CCCGGCCCCC GCTGTCCCTG GTGTAAAGAA
201 GTCGCCGTAG CCGTCGCGGC CGGGACTCCC CGGGCTCTCG CCCTTCAGGT
251 TTCGTTGACA CTCAGGACCG TACGTACGCT GCGCCATGTT CAAGAACTG
301 AAGCAAAGA TCAGCGAGGA GCAGCAGCAG CTCCAGCAGG CGCTGGCTCC
351 TGCTCAGGCG TCCTCCAATT CTTCAACACC AACAGAATG AGGAGCAGGA
401 CATCTTCATT TACAGAGCAA CTTGATGAAG GTACACCCAA TAGAGAGAAT
451 GCATCTACTC ATGCCTCGAA ATCTCCTGAC AGTGTTAATG GAAGTGAACC
501 AAGCATTCC T CAGTCAGGTG ACACACAGTC TTTTGCACAG AAGCTCCAGC
551 TCCGGGTGCC CTCCGTGGAG TCTTTGTTTC GAAGTCCGAT AAAGGAATCT
601 CTATTCCGGT CTTCTTCTAA AGAGTCTTTG GTACGAACAT CTTCCAGAGA
651 ATCCCTGAAT CGACTTGACC TGGACAGTTC TACTGCCAGT TTTGATCCAC
701 CCTCTGATAT GGATAGCGAG GCTGAAGACT TGGTAGGGAA TTCAGACAGT
751 CTCAACAAAG AACAGTTGAT TCAGCGGTTG CGAAGAATGG AACGAAGCTT
801 AAGTAGCTAC AGGGGAAAAT ATTCTGAGCT TGTTACAGCT TATCAGATGC
851 TTCAGAGAGA GAAGAAAAAG CTACAAGGTA TATTAAGTCA GAGTCAGGAT
901 AAATCACTTC GGAGAATAGC AGAATTAAGA GAGGAGCTCC AAATGGACCA
951 GCAGGCAAAG AACATCTG C AAGAGGAGTT TGATGCATCT TTAGAGGAGA
1001 AAGATCAGTA TATCAGTGTT CTCCAAACTC AGGTTTCTCT ACTGAAACAA
1051 CGATTACGAA ATGGCCCGAT GAATGTTGAT GTACTGAAAC CACTTCCTCA
1101 GCTGGAACCA CAGGCTGAAG TCTTCACTAA AGAAGAGAAT CCAGAAAGTG
1151 ATGGAGAGCC AGTAGTGGAA GATGGAAC TTCTGTAAGGA
1201 CTCCAGCAAA GAGTGAAGCG TCAAGAGAAC CTACTTAAGC GTTGTAAAGGA
1251 AACAAATTCAG TCACATAAGG AACAAATGTAC ACTATTAAGT AGTGAAGGAA
1301 AAGCTCTGCA AGAACAACTG GATGAAAGAC TTCAAGAACT AGAAAAGATA
1351 AAGGACCTTC ATATGGCCGA GAAGACTAAA CTTATCACTC AGTTGCGTGA
1401 TGCAAAGAAC TTAATTGAAC AGCTTGAACA AGATAAGGGA ATGGTAATCG
1451 CAGAGACAAA ACGTCAGATG CATGAAACCC TGGAAATGAA AGAAGAAGAA
1501 ATTGCTCAAC TCCGTAGTCG CATCAAACAG ATGACTACCC AGGGAGAGGA
1551 ATTACGGGAA CAGAAAGAAA AGTCCGAAAG AGCTGCTTTT GAGGAACTTG
1601 AAAAAGCTTT GAGTACAGCC CAAAAACAG AGGAAGCACG GAGAAAAGTG
1651 AAGGCAGAAA TGGATGAACA AATAAAACT ATCGAAAAAA CAAGTGAGGA
1701 GGAACGCATC AGTCTTCAAC AGGAATTAAG TCGGGTGAAA CAGGAGGTTG
1751 TTGATGTAAT GAAAAATCC TCAGAAGAAC AAATTGCTAA GCTACAGAAG
1801 CTTCATGAAA AGGAGCTGGC CAGAAAAGAG CAGGAACTGA CCAAGAAGCT
1851 TCAGACCCGA GAAAGGGAAT TTCAGGAACA AATGAAAGTA GCTCTTGAAA
1901 AGAGTCAATC AGAATATTTG AAGATCAGCC AAGAAAAAGA ACAGCAAGAA
1951 TCTTTGGCCC TAGAAGAGTT AGAGTTGCAG AAAAAAGCAA TCCTCACAGA
2001 AAGTGAAAAT AAAC TTCGGG ACCTTCAGCA AGAAGCAGAG ACTTACAGAA
2051 CTAGAATTCT TGAATTGGAA AGTTCTTTGG AAAAAAGCTT ACAAGAAAAC
2101 AAAAACTAGT CAAAAGATT GGCTGTTTCT CTGGAAGCTG AAAAAATAA
2151 GCACAATAAG GAGATTACAG TCATGGTTGA AAAACACAAG ACAGAATTGG
2201 AAAGCCTTAA GCATCAGCAG GATGCCCTTT GGACTGAAAA ACTCCAAGTC
2251 TTAAAGCAAC AATATCAGAC TGAAATGGAA AAACCTAGGG AAAAGTGTGA
2301 ACAAGAAAAA GAAACATTGT TGAAAGACAA AGAGATTATC TTCCAGGCCC
2351 ACATAGAAGA AATGAATGAA AAGACTTTAG AAAAGCTTGA TGTGAAGCAA
2401 ACAGAAGTAG AATCATTATC TTCTGAACTG TCAGAAGTAT TAAAGCCCCG
2451 TCACAAACTA GAAGAGGAAC TTTCTGTTCT GAAAGATCAA ACAGATAAAA
2501 TGAAGCAGGA ATTAGAGGCC AAGATGGATG AACAGAAAAA TCATCACCAG

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2551	CAGCAAGTTG	ACAGTATCAT	TAAAGAACAC	GAGGTATCTA	TCCAGAGGAC
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2651	AAAGGGACAA	GCATTTGAAA	GAGCATCAGG	CTCATGTAGA	AAATTTAGAG
2701	GCAGATATTA	AAAGGTCCTGA	AGGGGAACTC	CAGCAGGCAT	CTGCTAAGCT
2751	GGACGTTTTT	CAGTCTTACC	AGAGTGCCAC	ACATGAGCAG	ACAAAAGCAT
2801	ATGAGGAACA	GTTGGCCCAA	TTGCAGCAGA	AGTTGTTGGA	TTTGGAACA
2851	GAAAGAATTC	TTCTTACCAA	ACAGGTTGCT	GAAGTTGAAG	CACAAAAGAA
2901	AGATGTTTGT	ACTGAGTTAG	ATGCTCACAA	AATCCAGGTG	CAGGACTTAA
2951	TGCAGCAACT	TGAAAAACAA	AAAGTGAAA	TGGAGCAAAA	AGTAAAATCT
3001	TTAACCCAAAG	TCTATGAGTC	CAAACCTGAA	GATGGTAACA	AAGAACAGGA
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3101	GAGAAGGACA	GAAGAAAGAA	ATTGAGATAC	TCACACAGAA	ATTGTCAGCC
3151	AAGGAGGACA	GTATTCATAT	TTTGAATGAG	GAATATGAAA	CCAAATTTAA
3201	AAACCAAGAA	AAAAAGATGG	AAAAAGTTAA	GCAGAAAGCA	AAGGAGATGC
3251	AAGAAACGTT	AAAGAAAAAA	TTACTGGATC	AGGAAGCCAA	ACTTAAGAAA
3301	GAGCTTGAAA	ATACTGCTCT	AGAGCTTAGT	CAGAAAGAAA	AACAGTTTAA
3351	TGCCAAAATG	CTGGAAATGG	CACAGGCTAA	CTCAGCTGGA	ATCAGTATG
3401	CAGTGTCAAG	ACTGGAAACA	AACCAAAAAG	AACAAATAGA	AAGTCTTACT
3451	GAGGTTTCATC	GACGAGAACT	CAATGATGTC	ATATCAATCT	GGGAAAAGAA
3501	ACTTAATCAG	CAAGCTGAAG	AACTTCAGGA	AATACATGAA	ATCCAATTAC
3551	AGGAAAAAGA	ACAAGAGGTA	GCAGAACTGA	AACAAAAGAT	CCTCCTATTT
3601	GGGTGTGAAA	AAGAAGAGAT	GAACAAGGAA	ATAACATGGC	TGAAGGAAGA
3651	AGGTGTTAAG	CAGGATACAA	CATTAAATGA	ATTACAGGAA	CAGTTAAAGC
3701	AGAAGTCTGC	CCATGTGAAT	TCTCTTGCAC	AAGATGAAAC	TAAACTGAAA
3751	GCTCATCTTG	AAAAGCTAGA	GGTTGACTTG	AATAAGTCTC	TGAAGGAAAA
3801	TACTTTTCTT	CAAGAGCAGC	TAGTTGAACT	GAAGATGCTG	GCAGAAGAAG
3851	ATAAGCGGAA	GGTTTCTGAG	TTGACTAGCA	AGTTGAAAAC	CACAGATGAA
3901	GAATTCCAGA	GTTTGAAATC	TTACATGAA	AAAAGTAACA	AAAGCCTAGA
3951	GGACAAGAGC	TTGGAATTTA	AAAAACTGTC	TGAGGAACTA	GCGATT CAGC
4001	TAGATATTTG	CTGTAAGAAA	ACCGAAGCCT	TATTAGAAGC	TAAAACAAAT
4051	GAGCTAATCA	ACATTAGTAG	TAGTAAACT	AATGCCATTC	TTTCTAGGAT
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4151	AAACTTGCAC	AGTTTCTGAA	TTAGAAGCAC	AACTTAGACA	GTTGACAGAG
4201	GAGCAAAATA	CACTAAATAT	TTCTTTTCAA	CAGGCTACTC	ATCAGTTAGA
4251	AGAAAAAGAA	AATCAAATTA	AGAGCATGAA	GGCTGATATT	GAAAGTCTTG
4301	TAACAGAAAA	AGAAGCCTTA	CAGAAGGAAG	GAGGCAATCA	GCAACAGGCT
4351	GCTTCTGAAA	AGGAGTCTTG	TATAACACAG	TTGAAGAAAG	AGTTATCTGA
4401	AAACATCAAT	GCTGTCACAT	TGATGAAAGA	AGAGCTTAAA	GAAAAAAAAG
4451	TTGAGATTAG	CAGTCTTAGT	AAACAACTAA	CTGATTTGAA	TGTT CAGCTT
4501	CAAAATAGCA	TCAGCCTATC	CGAAAAAGAA	GCAGCCATTT	CATCACTAAG
4551	AAAGCAGTAT	GATGAAGAAA	AATGTGAATT	GCTGGATCAG	GTGCAAGATT
4601	TATCTTTTAA	AGTTGACACT	CTGAGTAAAG	AGAAAATTTT	TGCTCTTGAG
4651	CAGGTAGATG	ACTGGTCCAA	TAAATTCTCA	GAATGGAAGA	AGAAAGCACA
4701	GTCAAGATTT	ACACAGCATC	AAAACACTGT	TAAAGAATTG	CAGATCCAGC
4751	TTGAGTTAAA	ATCAAAGGAA	GCTTATGAAA	AGGATGAGCA	GATAAATTTA
4801	TTGAAGGAAG	AGCTTGATCA	GCAAAATAAA	AGATTTGATT	GTTTAAAGGG
4851	TGAAATGGAA	GACGACAAGA	GCAAGATGGA	GAAAAAGGAG	TCTAATTTAG
4901	AAACAGAGTT	AAAGTCTCAA	ACAGCAAGAA	TTATGGAATT	AGAGGACCAT
4951	ATTACCCAGA	AAACTATTGA	AATAGAGTCC	TTAAATGAAG	TTCTTAAAAA
5001	TTACAATCAA	CAAAAGGATA	TTGAACACAA	AGAATTGGTT	CAGAACTTTC
5051	AACATTTTCA	AGAGTTAGGA	GAAGAAAAGG	ACAACAGGGT	TAAAGAAGCT
5101	GAAGAAAAAA	TCTTAACACT	TGAAAACCAA	GTTTATTCCA	TGAAAGCTGA
5151	ACTTGAAACT	AAGAAGAAAG	AATTAGAACA	TGTGAATTTA	AGTGTGAAAA
5201	GCAAGAGGGA	GGAGTTAAAG	GCATTGGAAG	ATAGGCTTGA	GTCAGAAAGT

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5251 GCTGCAAAAT TAGCAGAGTT GAAGAGAAAA GCTGAACAAA AAATTGCTGC
5301 CATTAAGAAG CAGTTGTTAT CTCAAATGGA AGAGAAAAGAA GAACAGTATA
5351 AAAAAGGTAC AGAAAGCCAT TTGAGTGAGC TAAATACAAA ATTGCAGGAA
5401 AGAGAAAGGG AAGTTCACAT CTTGGAAGAA AAACCTAAGT CAGTGGAAGG
5451 TTCACAGTCA GAAACATTAA TTGTACCCAG ATCAGCAAAA AATGTGGCAG
5501 CATATACTGA ACAAGAAGAA GCAGATTCCC AAGGCTGTGT GCAGAAGACA
5551 TATGAAGAAA AAATCAGTGT TTTACAAAGA AACTTAACTG AAAAAGAAAA
5601 GCTATTGCAG AGGGTAGGGC AGGAAAAAGA AGAGACAGTT TCTTCTCATT
5651 TTGAAATGCG ATGCCAATAC CAGGAGCGCT TAATAAAGCT AGAACATGCT
5701 GAGGCAAAGC AACATGAAGA TCAAAGTATG ATAGGTCATC TTCAAGAGGA
5751 GCTTGAAGAA AAAACAAGA AATATTCTTT GATAGTAGCC CAGCATGTGG
5801 AAAAAGAAGG AGGTAAAAAT AACATACAGG CAAAGCAAAA CTTGGAAGAA
5851 GTGTTTGACG ACGTCCAGAA AACCCTCCAG GAGAAGGAAC TAACCTGTCA
5901 GATTTTGGAG CAAAAGATAA AAGAGCTGGA TTCCTGCTTA GTAAGACAGA
5951 AAGAAGTACA TAGAGTTGAA ATGGAAGAGT TGACCTCAA ATATGAAAAA
6001 TTACAGGCTT TACAACAGAT GGATGGAAGA AATAAACCCA CAGAACTTTT
6051 GGAAGAAAAC ACTGAAGAAA AGTCCAAATC ACATTGGGTC CAACCCAAAT
6101 TGCTTAGTAA CATGGAAGCC CAGCACAATG ATCTGGAGTT TAAATTAGCC
6151 GGGGCAGAAC GGGAGAAACA GAACTGGGC AAGGAGATTG TTAGATTGCA
6201 GAAAGACCTT CGAATGTTGA GAAAGGAGCA TCAGCAAGAA TTGGAATAC
6251 TAAAGAAAGA ATATGATCAA GAAAGGGAAG AGAAAATCAA ACAGGAGCAG
6301 GAAGATCTTG AACTGAAGCA CAATTCCACA TTAAAACAGC TGATGAGGGA
6351 GTTTAATACA CAGCTGGCAC AAAAGGAACA AGAGCTGGAA ATGACCATAA
6401 AAGAACTAT CAATAAGGCC CAGGAGGTGG AGGCTGAACT TTTAGAAAGC
6451 CATCAAGAAG AGACAAATCA GTTACTTAAA AAAATTGCTG AGAAAGATGA
6501 TGATCTAAAA CGAACAGCCA AAAGATATGA AGAAATCCTT GATGCTCGTG
6551 AAGAAGAAAT GACTGCAAAA GTAAGGGACC TGCAGACTCA ACTTGAGGAG
6601 TGCAGAGA AATACCAGCA AAAGCTAGAG CAGGAGGAGA ACCCTGGCAA
6651 TGATAATGTA ACAATTATGG AGCTACAGAC ACAGCTAGCA CAGAAGACGA
6701 CTTTAATCAG TGATTCGAAA TTGAAAAGAGC AAGAGTTCAG AGAACAGATT
6751 CACAATTTAG AAGACCGTTT GAAGAAATAT GAAAAGAATG TATATGCAAC
6801 AACTGTGGGG ACACCTTACA AAGGTGGCAA TTTGTACCAT ACGGATGTCT
6851 CACTCTTTGG AGAACCTACC GAATTTGAGT ATTTGCGAAA AGTGCTTTTT
6901 GAGTATATGA TGGGTCGTGA GACTAAGACC ATGGCAAAAG TTATAACCAC
6951 CGTACTGAAG TTCCCTGATG ATCAGACTCA GAAAATTTTG GAAAGAGAAG
7001 ATGCTCGGCT GATGTTTACT TCACCTCGCA GTGGTATCTT CTGAGTAAAC
7051 CATCAGTCTG TGCTTAGTTA ACATGTGTCA TGGCTCCGAT CTTCATCTTG
7101 AAGAAGAGTG ACATTGGGTG ACTGCTGCTT GGAAAACGTG CCACACTTGC
7151 TACTCTTTGA GAATGAAGTT GTCATTGAGG GCCCCTCATG TAGCCAAAAG
7201 ACCAAGAAAA ATCTGGCCCA CAGATAAGTT GCAGACTGCC TTTAAATAG
7251 ATTTTATCAG TGGAGAAATG GTGATAGTTT TTTCTTCAGT TTTCTCTTGG
7301 GAAGAGTTTT ATGTTGTTTA AAAGATATTT TGATAACTTA ACCTGCTTTA
7351 TGGGCTTACA TAATATTCCT TTCATCCATT CTTTTTAAAG AACGGCTTAC
7401 CTTTCCTATT TATTTTTAGG GTGATTTTTT AAAAAGACTT GTGCAATACA
7451 TTTTGAGGTG AAACCTAGTG GATTTTTTCT GATAAATTAG AGCATTTAAT
7501 TGACTATTTT ATTCAGGTG ATCTGTTGAA TATTTGCTAA AGACCAGTTC
7551 TTTAAGCTAA GACATGTAAA AAATCCCAA TGGCAGTACC TCATTGTTTA
7601 CTTAGCTTTT GTACTTATAT TTTTCAGAGG AAAAACAAC ACTGTAAATT
7651 GTGAATAGCC AATACATAAC TGTATTGTAT GCAAATCTGT GATTGTTGGC
7701 AGTGTCTCT CTGAGAAACA GATAAATAAA GTTTATTTAC TAT

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Fig. 11: SEQ ID NO. 8: amino acid sequence of human golgin-245, splice variant 4**Length: 2252 aa**

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1  MFKKCLKQKIS EEQQQLQQAL APAQASSNSS TPTRMRSRTS SFTEQLDEGT
51  PNRENASTHA SKSPDSVNGS EPSIPQSGDT QSFAQKLQLR VPSVESLFRS
101 PIKESLFRSS SKESLVRTSS RESLNRLDLD SSTASFDPPS DMDSEAEDLV
151 GNSDSLNEQ LIQRLRRMER SLSSYRGKYS ELVTAYQMLQ REKKKLQGIL
201 SQSQDKSLRR IAELEELQM DQQAQKHLQE EFDASLEEKD QYISVLQTQV
251 SLLKQRLRNG PMNVDVLKPL PQLEPQAEVF TKEENPESDG EPVVEDGTSV
301 KTLETLQQRV KRQENLLKRC KETIQSHKEQ CTTLTSEKEA LQEQOLDERLO
351 ELEKIKDLHM AEKTKLITQL RDAKNLIEQL EQDKGMVIAE TKRQMHTLE
401 MKEEEIAQLR SRIKQMTTQG EELREQKEKS ERAAFEELEK ALSTAQKTEE
451 ARRKLKAEMD EQIKTIEKTS EEERISLQQE LSRVKQEVVD VMKKSSEEQI
501 AKLQKLHEKE LARKEQELTK KLQTREREFQ EQMKVALEKS QSEYLIKISQE
551 KEQQESLAE ELELQKKAIL TESENKLRLD QQAETRYRTR ILELESSLEK
601 SLQENKNQSK DLAVHLEAEK NKHNKEITVM VEKHKTELES LKHQQDALWT
651 EKLQVLKQOY QTEMEKLREK CEQEKETLLK DKEIIFQAH I EEMNEKTLEK
701 LDVKQTELES LSSEELSEVLK ARHKLEEEELS VLKDQTDKMK QELEAKMDEQ
751 KNHHQQQVDS I I KEHEVSIQ RTEKALKDQI NQLELLLLKER DKHLKEHQAH
801 VENLEADIKR SEGELQQASA KLDVFQSYQS ATHEQTKAYE EQLAQLQQKL
851 LDLETERILL TKQVAEVEAQ KKDVCTELDA HKIQVQDLMQ QLEKQNSEME
901 QKVKSILTQVY ESKLEDGNKE QEQTQKILVE KENMILQMR E GQKKEIEILT
951 QKLSAKEDSI HILNEEYETK FKNQEKKMEK VKQKAKEMQE TLKKKLLDQE
1001 AKLKKELENT ALELSQKEKQ FNAKMLEMAQ ANSAGISDAV SRLETNQKEQ
1051 IESLTEVHRR ELNDVISIWE KKLNQQAEE L QEIHEIQLQE KEQEVAELKQ
1101 KILLFGCEKE EMNKEITWLK EEGVKQDRTL NELQEQLKQK SAHVNSLAQD
1151 ETKLKAHLEK LEVDLNKSLK ENTFLQEQLV ELKMLAEEDK RKVSELTSKL
1201 KTTDEEFQSL KSSHEKSNKS LEDKSLEFKK LSEELAIQLD ICCKKTEALL
1251 EAKTNELINI SSSKTNAILS RISHCQHRTT KVKEALLIKT CTVSELEAQL
1301 RQLTEEQNTL NISFQQATHQ LEEKENQIKS MKADIESLVT EKEALQKEGG
1351 NQQQAASEKE SCITQLKKEL SENINAVTLM KEELKEKKVE ISSLSKQLTD
1401 LNVQLQNSIS LSEKEAAISS LRKQYDEEKC ELLDQVQDLS FKVDTLSEK
1451 ISALEQVDDW SNKFSEWKKK AQSRTQHQH TVKELQIQLE LKSKEAYEKD
1501 EQINLLKEEL DQQNKRFDCL KGEMEDDKSK MEKKESNLET ELKSQTARIM
1551 ELEDHITQKT IEIESLNEVL KNYNQQKDIE HKELVQKLQH FQELGEEKDN
1601 RVKEAEEKIL TLENQVYSMK AELETKKKEL EHVNLVSKS EEELKALED R
1651 LESESAAKLA ELKRKAEQKI AAIKKQLLSQ MEEKEEQYKK GTESHLSELN
1701 TKLQEREREV HILEEKLKSV ESSQSETLIV PRSAKNVAAY TEQEEADSQ
1751 CVQKTYEEKI SVLQRNLTEK EKLLQRVGQE KEETVSSHFE MRCQYQERLI
1801 KLEHAEAKQH EDQSMIGHLQ EELEEKNNKY SLIVAQHVEK EGGKNNIQAK
1851 QNLENVFDDV QKTLQEKELT CQILEQKIKE LDSCLVRQKE VHRVEMEELT
1901 SKYEKLQALQ QMDGRNKPTE LLEENTEEKS KSHLVQPKLL SNMEAQHNDL
1951 EFKLAGAERE KQKLGEIVR LQKDLRMLRK EHQQELEILK KEYDQEREK
2001 IKQEQEDLEL KHNSTLKQLM REFNTQLAQK EQELEM TIKE TINKAQEVEA
2051 ELLESHQEET NQLLKKIAEK DDDLKRTAKR YEEILDAREE EMTAKVRDLQ
2101 TQLEELQKKY QQKLEQEENP GNDNVTIMEL QTQLAQKTTL ISDSKLKEQE
2151 FREQIHNLED RLKKYEKNVY ATTVGTPYKG GNLYHTDVSL FGEPTFEFYL
2201 RKVLFYMMG RETKTMKVI TTVLKFPDDQ TQKILEREDA RLMFTSPRSG
2251 IF

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Fig. 12: SEQ ID NO. 9: nucleotide sequence of human golgin-245 cDNA, splice variant 4

Length: 7761 bp

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1   GCAACGAAGG TACCATGGCC GTTGTCTGTCG CCGCCGCGGC TCCCGGGGCT
51  GGATGGGGGG CCGAGGCCAG CCAGTGGCAC CCGGAAGAAA GAGACGCGGC
101 GGC GGCGACG CCGACACCCT CAGGACGAGT GTCCGGACTT GCCCAGAGCC
151 TCAAGGAGGA GACGGCGAGG CCCGGCCCCC GCTGTCCCTG GTGTAAAGAA
201 GTCGCCGTAG CCGTCGCGGC CGGGACTCCC CGGGCTCTCG CCCTTCAGGT
251 TTCGTTGACA CTCAGGACCG TACGTACGCT GCGCCATGTT CAAGAACTG
301 AAGCAAAAGA TCAGCGAGGA GCAGCAGCAG CTCCAGCAGG CGCTGGCTCC
351 TGCTCAGGCG TCCTCCAATT CTTCAACACC AACAAGAATG AGGAGCAGGA
401 CATCTTCATT TACAGAGCAA CTTGATGAAG GTACACCCAA TAGAGAGAAT
451 GCATCTACTC ATGCCTCGAA ATCTCCTGAC AGTGTTAATG GAAGTGAACC
501 AAGCATTCCCT CAGTCAGGTG ACACACAGTC TTTTGCACAG AAGCTCCAGC
551 TCCGGGTGCC CTCGGTGGAG TCTTTGTTTC GAAGTCCGAT AAAGGAATCT
601 CTATTCCGGT CTTCTTCTAA AGAGTCTTTG GTACGAACAT CTTCCAGAGA
651 ATCCCTGAAT CGACTTGACC TGGACAGTTC TACTGCCAGT TTTGATCCAC
701 CCTCTGATAT GGATAGCGAG GCTGAAGACT TGGTAGGGAA TTCAGACAGT
751 CTCAACAAAG AACAGTTGAT TCAGCGGTTG CGAAGAATGG AACGAAGCTT
801 AAGTAGCTAC AGGGGAAAAT ATTCTGAGCT TGTTACAGCT TATCAGATGC
851 TTCAGAGAGA GAAGAAAAG CTACAAGGTA TATTAAGTCA GAGTCAGGAT
901 AAATCACTTC GGAGAATAGC AGAATTAAGA GAGGAGCTCC AAATGGACCA
951 GCAGGCAAAG AAACATCTGC AAGAGGAGTT TGATGCATCT TTAGAGGAGA
1001 AAGATCAGTA TATCAGTGTT CTCCAACTC AGGTTTCTCT ACTGAAACAA
1051 CGATTACGAA ATGGCCCGAT GAATGTTGAT GTACTGAAAC CACTTCCTCA
1101 GCTGGAACCA CAGGCTGAAG TCTTCACTAA AGAAGAGAAT CCAGAAAGTG
1151 ATGGAGAGCC AGTAGTGGA GATGGAACCT CTGTAAAAAC ACTGGAAACA
1201 CTCCAGCAAA GAGTGAAGCG TCAAGAGAAC CTACTTAAGC GTTGTAAAGGA
1251 AACAAATCAG TCACATAAGG AACAAATGTAC ACTATTAACT AGTGAAAAAG
1301 AAGCTCTGCA AGAACAACTG GATGAAAGAC TTCAAGAACT AGAAAAGATA
1351 AAGGACCTTC ATATGGCCGA GAAGACTAAA CTTATCACTC AGTTGCGTGA
1401 TGCAAAGAAC TTAATTGAAC AGCTTGAACA AGATAAGGGA ATGGTAATCG
1451 CAGAGACAAA ACGTCAGATG CATCAAACAG ATGACTACCC AGGGAGAGGA
1501 ATTGCTCAAC TCCGTAGTCG CATCAAACAG ATGACTACCC AGGGAGAGGA
1551 ATTACGGGAA CAGAAAGAAA AGTCCGAAAG AGCTGCTTTT GAGGAACTTG
1601 AAAAAGCTTT GAGTACAGCC CAAAAACAG AGGAAGCAGG GAGAAACTTG
1651 AAGGCAGAAA TGGATGAACA AATAAAACT ATCGAAAAAA CAAGTGAGGA
1701 GGAACGCATC AGTCTTCAAC AGGAATTAAG TCGGGTGAAA CAGGAGGTTG
1751 TTGATGTAAT GAAAAAATCC TCAGAAGAAC AAATTGCTAA GCTACAGAAG
1801 CTTTATGAAA AGGAGCTGGC CAGAAAAGAG CAGGAACTGA CCAAGAAGCT
1851 TCAGACCCGA GAAAGGGAAT TTCAGGAACA AATGAAAGTA GCTCTTGAAA
1901 AGAGTCAATC AGAATATTTG AAGATCAGCC AAGAAAAAGA ACAGCAAGAA
1951 TCTTTGGCCC TAGAAGAGTT AGAGTTGCAG AAAAAAGCAA TCCTCACAGA
2001 AAGTGAAAAT AAACCTCGGG ACCTTCAGCA AGAAGCAGAG ACTTACAGAA
2051 CTAGAATTCT TGAATTGGAA AGTTCTTTGG AAAAAAGCTT ACAAGAAAAC
2101 AAAAATCAGT CAAAAGATTT GGCTGTTTCT CTGGAAGCTG AAAAAATAA
2151 GCACAATAAG GAGATTACAG TCATGGTTGA AAAACACAAG ACAGAATTGG
2201 AAAGCCTTAA GCATCAGCAG GATGCCCTTT GGACTGAAAA ACTCCAAGTC
2251 TTAAAGCAAC AATATCAGAC TGAAATGGAA AAAGTTAGGG AAAAGTGTGA
2301 ACAAGAAAAA GAAACATTGT TGAAAGACAA AGAGATTATC TTCCAGGCCC
2351 ACATAGAAGA AATGAATGAA AAGACTTTAG AAAAGCTTGA TGTGAAGCAA
2401 ACAGAACTAG AATCATTATC TTCTGAACTG TCAGAAGTAT TAAAAGCCCG
2451 TCACAAACTA GAAGAGGAAC TTTCTGTTCT GAAAGATCAA ACAGATAAAA
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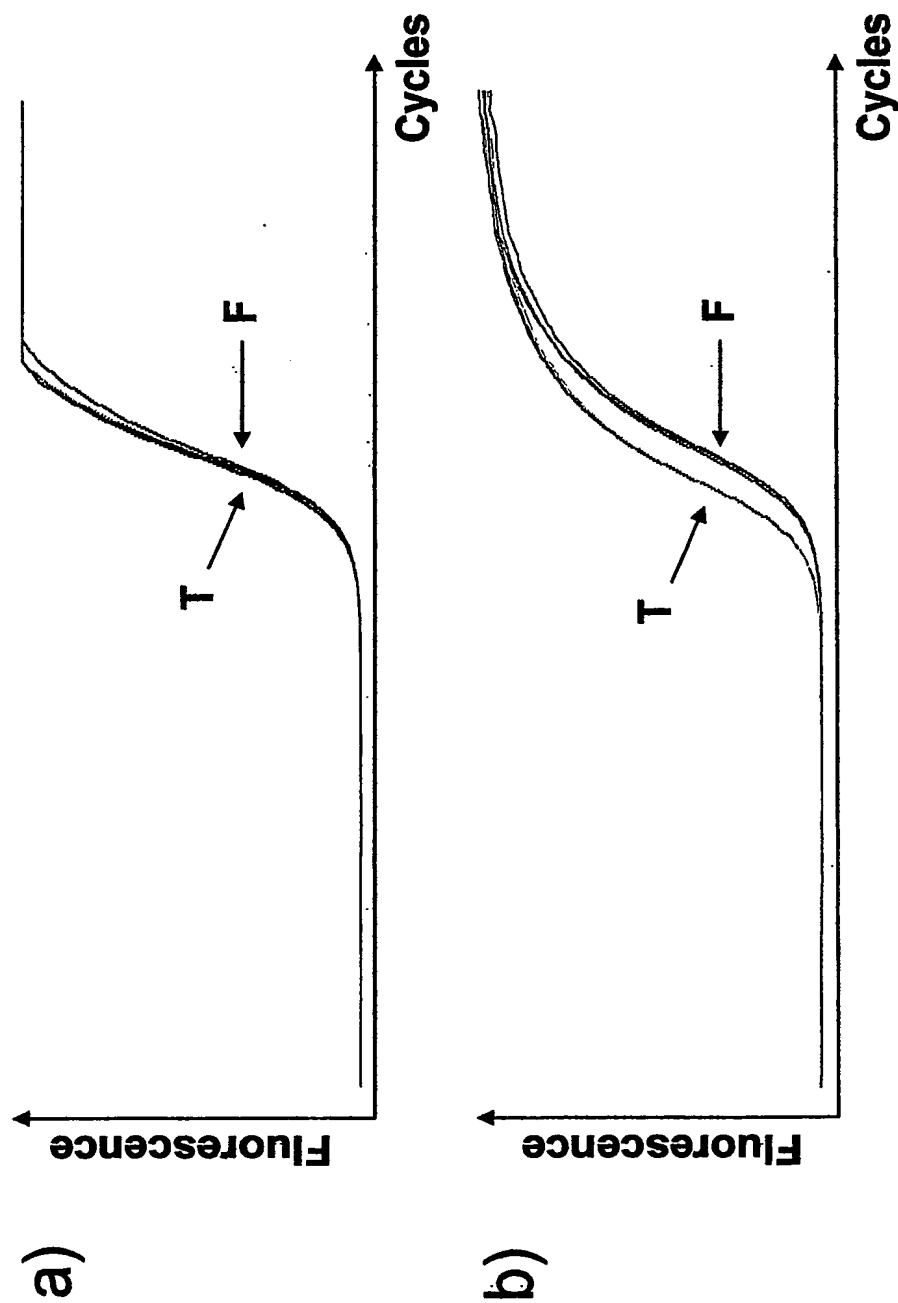
2501	TGAAGCAGGA	ATTAGAGGCC	AAGATGGATG	AACAGAAAAA	TCATCACCAG
2551	CAGCAAGTTG	ACAGTATCAT	TAAAGAACAC	GAGGTATCTA	TCCAGAGGAC
2601	TGAGAAGGCA	TTAAAAGATC	AAATTAATCA	ACTTGAGCTT	CTCTTGAAGG
2651	AAAGGGACAA	GCATTTGAAA	GAGCATCAGG	CTCATGTAGA	AAATTTTAGAG
2701	GCAGATATTA	AAAGGTCTGA	AGGGGAACTC	CAGCAGGCAT	CTGCTAAGCT
2751	GGACGTTTTT	CAGTCTTACC	AGAGTGCCAC	ACATGAGCAG	ACAAAAGCAT
2801	ATGAGGAACA	GTTGGCCCAA	TTGCAGCAGA	AGTTGTTGGA	TTTGGAAACA
2851	GAAAGAATTC	TTCTTACCAA	ACAGGTTGCT	GAAGTTGAAG	CACAAAAGAA
2901	AGATGTTTGT	ACTGAGTTAG	ATGCTCACAA	AATCCAGGTG	CAGGACTTAA
2951	TGCAGCAACT	TGAAAAACAA	AATAGTGAAA	TGGAGCAAAA	AGTAAAATCT
3001	TTAACCCAAG	TCTATGAGTC	CAAACTTGAA	GATGGTAACA	AAGAACAGGA
3051	ACAGACAAAG	CAAATCTTGG	TGGAAAAGGA	AAATATGATT	TTACAAATGA
3101	GAGAAGGACA	GAAGAAAGAA	ATTGAGATAC	TCACACAGAA	ATTGTCAGCC
3151	AAGGAGGACA	GTATTCATAT	TTTGAATGAG	GAATATGAAA	CCAAATTTAA
3201	AAACCAAGAA	AAAAAGATGG	AAAAAGTTAA	GCAGAAAGCA	AAGGAGATGC
3251	AAGAAACGTT	AAAGAAAAAA	TTACTGGATC	AGGAAGCCAA	ACTTAAAGAA
3301	GAGCTTGAAA	ATACTGCTCT	AGAGCTTAGT	CAGAAAGAAA	AACAGTTTAA
3351	TGCCAAAATG	CTGGAAATGG	CACAGGCTAA	CTCAGCTGGA	ATCAGTGTAG
3401	CAGTGTCAAG	ACTGGAAACA	AACCAAAAAG	AACAAATAGA	AAGTCTTACT
3451	GAGGTTTCATC	GACGAGAACT	CAATGATGTC	ATATCAATCT	GGGAAAAGAA
3501	ACTTAATCAG	CAAGCTGAAG	AACCTCAGGA	AATACATGAA	ATCCAATTAC
3551	AGGAAAAAGA	ACAAGAGGTA	GCAGAACTGA	AACAAAAGAT	CCTCCTATTT
3601	GGGTGTGAAA	AAGAAGAGAT	GAACAAGGAA	ATAACATGGC	TGAAGGAAGA
3651	AGGTGTTAAG	CAGGATACAA	CATTAAATGA	ATTACAGGAA	CAGTTAAAGC
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4101	TTCTCATTGT	CAGCACCGTA	CAACTAAAGT	TAAGGAGGCA	CTGTTAATTA
4151	AACTTGCAC	AGTTTCTGAA	TTAGAAGCAC	AACTTAGACA	GTTGACAGAG
4201	GAGCAAAATA	CACTAAATAT	TTCTTTTCAA	CAGGCTACTC	ATCAGTTAGA
4251	AGAAAAAGAA	AATCAAATTA	AGAGCATGAA	GGCTGATATT	GAAAGTCTTG
4301	TAACAGAAAA	AGAAGCCTTA	CAGAAGGAA	GAGGCAATCA	GCAACAGGCT
4351	GCTTCTGAAA	AGGAGTCTTG	TATAACACAG	TTGAAGAAAG	AGTTATCTGA
4401	AAACATCAAT	GCTGTCACAT	TGATGAAAGA	AGAGCTTAAA	GAAAAAAAAG
4451	TTGAGATTAG	CAGTCTTAGT	AAACAACATA	CTGATTTGAA	TGTTTCAGCTT
4501	CAAAATAGCA	TCAGCCTATC	CGAAAAAGAA	GCAGCCATTT	CATCACTAAG
4551	AAAGCAGTAT	GATGAAGAAA	AATGTGAATT	GCTGGATCAG	GTGCAAGATT
4601	TATCTTTTAA	AGTTGACACT	CTGAGTAAAG	AGAAAATTTT	TGCTCTTGAG
4651	CAGGTAGATG	ACTGGTCCAA	TAAATTCTCA	GAATGGAAGA	AGAAAGCACA
4701	GTCAAGATTT	ACACAGCATC	AAAACACTGT	TAAAGAATTG	CAGATCCAGC
4751	TTGAGTTAAA	ATCAAAGGAA	GCTTATGAAA	AGGATGAGCA	GATAAATTTA
4801	TTGAAGGAAG	AGCTTGATCA	GCAAAATAAA	AGATTTGATT	GTTTAAAGGG
4851	TGAAATGGAA	GACGACAAGA	GCAAGATGGA	GAAAAAGGAG	TCTAATTTAG
4901	AAACAGAGTT	AAAGTCTCAA	ACAGCAAGAA	TTATGGAATT	AGAGGACCAT
4951	ATTACCCAGA	AAACTATTGA	AATAGAGTCC	TTAAATGAAG	TTCTTAAAAA
5001	TTACAATCAA	CAAAAGGATA	TTGAACACAA	AGAATTGGTT	CAGAACTTTC
5051	AACATTTTCA	AGAGTTAGGA	GAAGAAAAGG	ACAACAGGGT	TAAAGAAGCT
5101	GAAGAAAAAA	TCTTAACACT	TGAAAACCAA	GTTTATTCCA	TGAAAGCTGA
5151	ACTTGAAACT	AAGAAGAAAG	AATTAGAACA	TGTGAATTTA	AGTGTGAAAA

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5201 GCAAAGAGGA GGAGTTAAAG GCATTGGAAG ATAGGCTTGA GTCAGAAAGT
5251 GCTGCAAAAT TAGCAGAGTT GAAGAGAAAA GCTGAACAAA AAATTGCTGC
5301 CATTAAGAAG CAGTTGTTAT CTCAAATGGA AGAGAAAGAA GAACAGTATA
5351 AAAAAGGTAC AGAAAGCCAT TTGAGTGAGC TAAATACAAA ATTCAGGAA
5401 AGAGAAAGGG AAGTTCACAT CTTGGAAGAA AAACCTAAGT CAGTGGAAG
5451 TTCACAGTCA GAAACATTAA TTGTACCCAG ATCAGCAAAA AATGTGGCAG
5501 CATATACTGA ACAAGAAGAA GCAGATTCCC AAGGCTGTGT GCAGAAGACA
5551 TATGAAGAAA AAATCAGTGT TTTACAAAGA AACTTAACTG AAAAAGAAAA
5601 GCTATTGCAG AGGGTAGGGC AGGAAAAAGA AGAGACAGTT TCTTCTCATT
5651 TTGAAATGCG ATGCCAATAC CAGGAGCGCT TAATAAAGCT AGAACATGCT
5701 GAGGCAAAGC AACATGAAGA TCAAAGTATG ATAGGTCATC TTCAAGAGGA
5751 GCTTGAAGAA AAAACAAGA AATATTCCTT GATAGTAGCC CAGCATGTGG
5801 AAAAGAAGG AGGTAAAAAT AACATACAGG CAAAGCAAAA CTTGGAAAAAT
5851 GTGTTTGACG ACGTCCAGAA AACCCCTCCAG GAGAAGGAAC TAACCTGTCA
5901 GATTTTGGAG CAAAAGATAA AAGAGCTGGA TTCCTGCTTA GTAAGACAGA
5951 AAGAAGTACA TAGAGTTGAA ATGGAAGAGT TGACCTCAA ATATGAAAAA
6001 TTACAGGCTT TACAACAGAT GGATGGAAGA AATAAACCCA CAGAACTTTT
6051 GGAAGAAAA ACTGAAGAAA AGTCCAAATC ACATTTGGTC CAACCCAAAT
6101 TGCTTAGTAA CATGGAAGCC CAGCACAATG ATCTGGAGTT TAAATTAGCC
6151 GGGGAGAAAC GGGAGAAACA GAAACTGGGC AAGGAGATTG TTAGATTGCA
6201 GAAAGACCTT CGAATGTTGA GAAAGGAGCA TCAGCAAGAA TTGGAAATAC
6251 TAAAGAAAGA ATATGATCAA GAAAGGGAAG AGAAAATCAA ACAGGAGCAG
6301 GAAGATCTTG AACTGAAGCA CAATTCACA TTA AACAGC TGATGAGGGA
6351 GTTTAATACA CAGCTGGCAC AAAAGGAACA AGAGCTGGAA ATGACCATAA
6401 AAGAACTAT CAATAAGGCC CAGGAGGTGG AGGCTGAACT TTTAGAAAGC
6451 CATCAAGAAG AGACAAATCA GTTACTTAAA AAAATTGCTG AGAAAGATGA
6501 TGATCTAAAA CGAACAGCCA AAAGATATGA AGAAATCCTT GATGCTCGTG
6551 AAGAAGAAAT GACTGCAAAA GTAAGGGACC TGCAGACTCA ACTTGAGGAG
6601 CTGCAGAAGA AATACCAGCA AAAGCTAGAG CAGGAGGAGA ACCCTGGCAA
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6701 CTTTAATCAG TGATTTCGAA TTGAAAGAGC AAGAGTTCAG AGAACAGATT
6751 CACAATTTAG AAGACCGTTT GAAGAAATAT GAAAAGAATG TATATGCAAC
6801 AACTGTGGGG ACACCTTACA AAGGTGGCAA TTTGTACCAT ACGGATGTCT
6851 CACTCTTTGG AGAACCTACC GAATTTGAGT ATTTGCGAAA AGTGCTTTTTT
6901 GAGTATATGA TGGGTCGTGA GACTAAGACC ATGGCAAAAG TTATAACCAC
6951 CGTACTGAAG TTCCCTGATG ATCAGACTCA GAAAATTTTG GAAAGAGAAG
7001 ATGCTCGGCT GATGTTTACT TCACCTCGCA GTGGTATCTT CTGAGTAAAC
7051 CATCAGTCTG TGCTTAGTTA ACATGTGTCA TGGCTCCGAT CTTCATCTTG
7101 AAGAAGAGTG ACATTGGGTG ACTGCTGCTT GGAAAACGTG CCACACTTGC
7151 TACTCTTTGA GAATGAAGTT GTCATTGAGG GCCCCTCATG TAGCCAAAAG
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7451 ATTTTGAGGT GAAACTTAGT GGATTTTTTC TGATAAATTA GAGCATTTAA
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7551 CTTTAAGCTA AGACATGTAA AAAATCCCAA ATGGCAGTAC CTCATTGTTT
7601 ACTTAGCTTT TGTACTTATA TTTTTCAGAG GAAAAACAC TACTGTAAAT
7651 TGTGAATAGC CAATACATAA CTGTATTGTA TGCAAATCTG TGATTGTTGG
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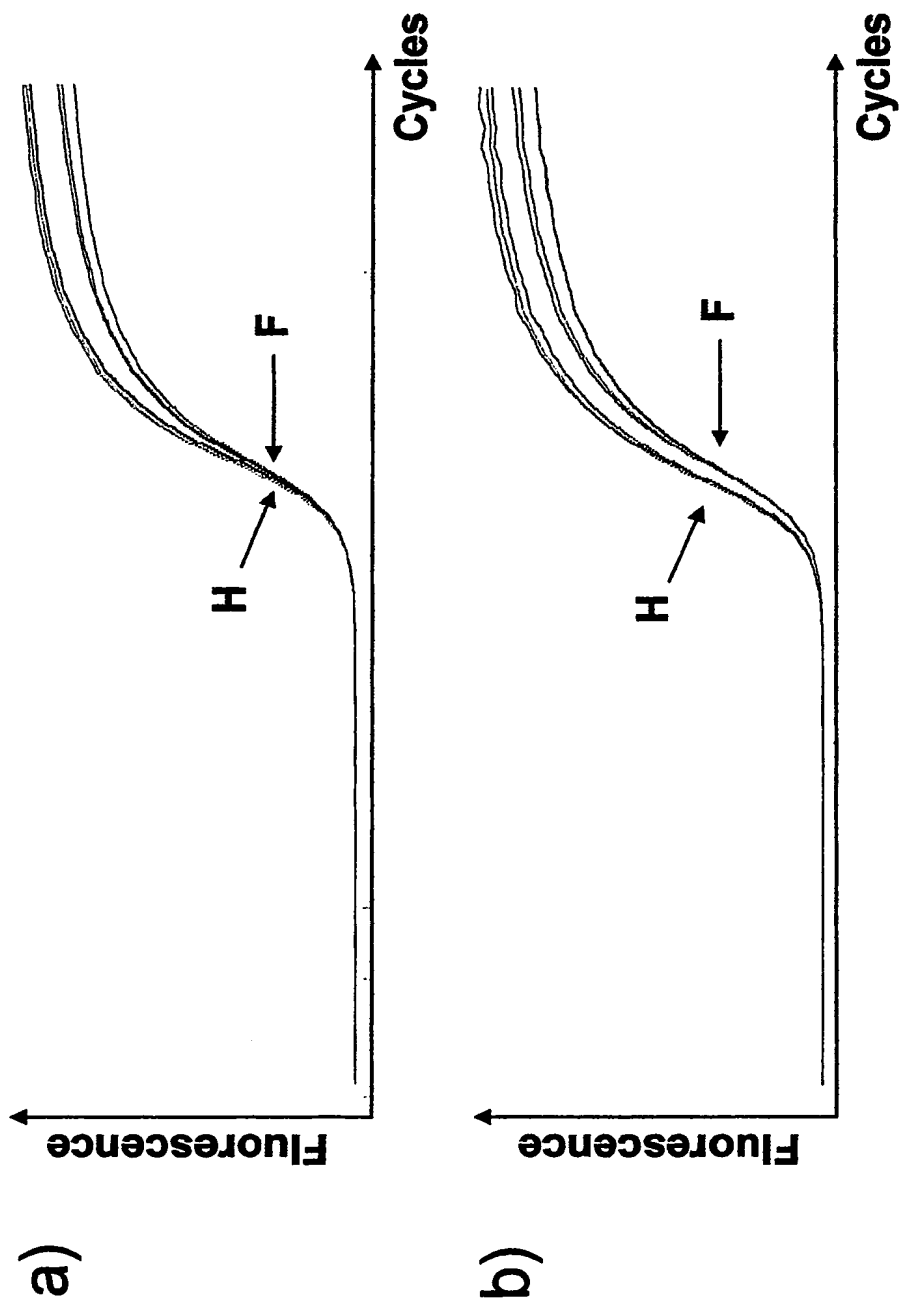
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Fig. 13: Verification of differential expression of golgin-245 splice variant 1 and/or 3 by quantitative RT-PCR

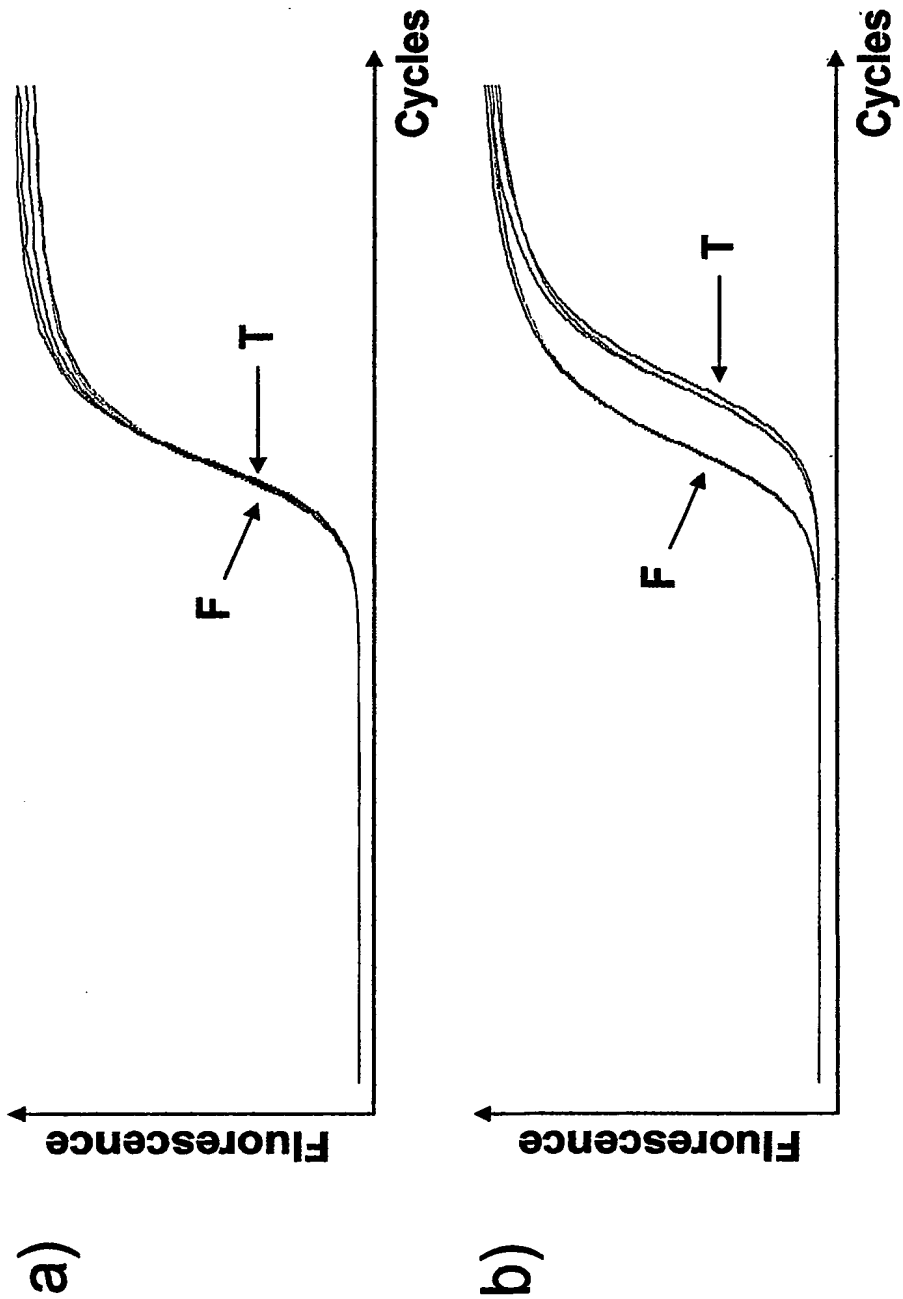


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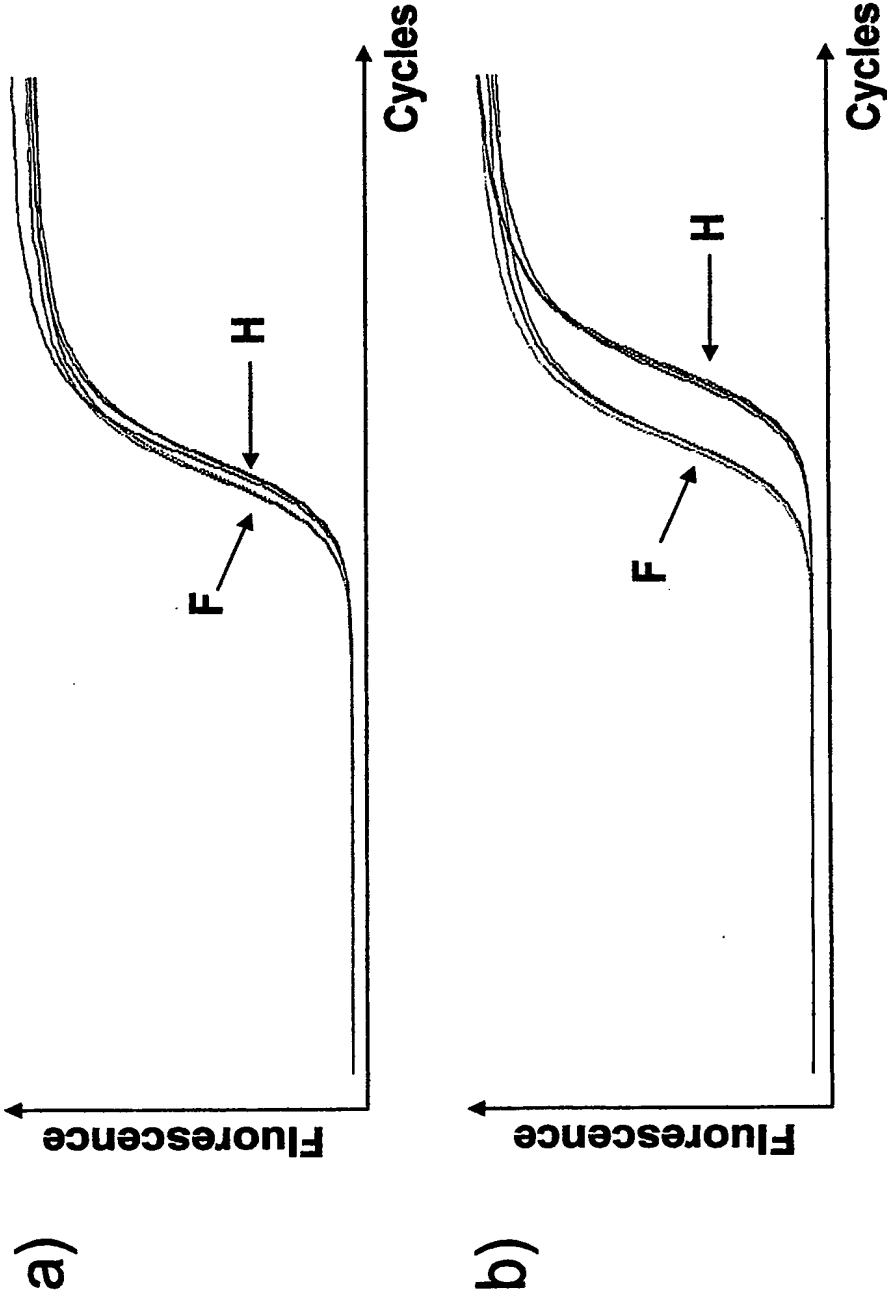
**Fig. 14: Verification of differential expression
of golgin-245 splice variant 1 and/or 3
by quantitative RT-PCR**



**Fig. 15: Verification of differential expression
of golgin-245 splice variant 2 and/or 4
by quantitative RT-PCR**



**Fig. 16: Verification of differential expression
of golgin-245 splice variant 2 and/or 4
by quantitative RT-PCR**



**Fig. 17: Images of the human cerebral cortex
labeled with anti-golgin-245 monoclonal
antibody and with DAPI**

